

FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESIC SARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDCGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLRLRQSP
RAFIPPAFVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

FIGURE 88

GGCGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGA
TATTGACAACTGAAGCTTTCTGCACTGGACTTAAGGAAGAGTGTACTCGTAGGCCGA
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAAGAGCAGAGTCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCTCCACGAATGGGAAGGTTTTATTGAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGTCCAAAGAGCTCTTAAAGCTTGCAGAAATTTT
ATCCAACCTTGTGTTGGAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCCTGGTTT
CATAGTCCAAGCGGAGATCCTACTGGCAGAGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTCATTACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTCTCATGATAATGGCAGCCAGTTTTTCTTCACTGGGTCGAGCAGATGAAC
TAACAATAAGCATAACATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAGCTGT
GAGGTTTTGTTAATCCTTTTGTATGACATCATTTCAAGGGAAATTAAGGCTGAAAAAGA
GAAACAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTCCAGT
TGTAAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAAATTAACGGGAACCTTTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAGAAAGTGAAGAGGAAGAA
GCCCTCCAGATGGTGTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACAGT
TTAAATCTAACTCACTCAAGCAATTGCTGAAAACACCTGAAAATGACATTCCTGAAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA
ATAAAGGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAAT
GAGAATAATGATAAACAGAACTTGCTGGAAATGTGCCTACAATGGCCCTTGTAAACAGCCATTG
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTTG
AAAAACAATTATCTTGTGTTTGCATAATGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTGG
TACATGTGTTTTTCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTTCCT
TCCACAAAAA

FIGURE 1

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATCCCCGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGTGGCCCCACCACCCGAGG
AGCAGCTCCTGCCCTGTCCGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGTGTGTGTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCGCTTAGGGTGTGTGCT
GTCCCGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTCC
TCACCACCTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATTTATAGGACCGCTAC
CGCCGACGCTTGGGCTGGCCCTGCCAGGCTCGCTACGCGTGTGCCCCGGCTGGAAGAG
GACCAGCGGGCTTCTTGGGCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCTGGCCGCTGCCGCTGCCCTGCAGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTAGGAGGGGCGGCTGTCCCAGCGCTGCATCAACACCGC
CGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCTGTCTGCAGACGTTACACTCTGTG
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGTGCAGCTGGTGT
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGCAGCC
TCCTGGTGCACTCCTTCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCTTTC
CTGGAGGAGCAGCTGGGCTCTGCTCCTGCAAGAAAGACTCGTGACTGCCCCAGCGCCCCAGG
CTGGACTGAGCCCCCTCAGCCCGCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTTTTCTCTCTC
CCCTTCCCTCGGGAGGGTCCCCAGACCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCCAACGGCATCCCAAGGCCAGGTGGGCCCCFA
GCTGAGGGAAGGTACAGATTCCCTGCTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCTCAGTGGGGCTGTGCTGCTGACCCCCAGCACAAATAAATGAAA
CGTGAAAAAAGGGCGGCCGACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCACTGTGTTATGTCAGCTTATAATGGT
TACAAAT

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FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCFAGWRGDTCSQSDVDECSARRGGCPQRCINTAGSYWCQCW
EGHSLSDGTLTCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLEPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG
 GTCAGCCCCACGGCGGGGACATATGGTGAAATTCCCCGGCGCTCAGCAGCTACTTGGCCCCCTGATC
 CGGTTCTTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
 ACTCCCTCATGAAGTCTTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCCTGGTGTTT
 GTGAACAGCAAGAGAGACAGGACCAAAAGCCGCTCTGTATGGTGGTGGCAGGGCCATCGC
 TGCCGTCTTTCACACACTGTAGCTTATAGTGATTTAGGATACATACATTATCAATAAATCTGC
 ACCATGTGGCAGTGTCGGTGGGGAGCAAGACGAGAAGGGCCCTTCGTACTCTCGTCCGCGCTTT
 CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAAACAAATACAGTTT
 CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC
 TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCTCTCCTTGTACATGGGC
 GCACTTGTGCGCTGCACCACCCCTGTGCTGGGCTACTACAAGAACATTCACGACATCATCCC
 TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT
 GGCCCTTTGGCTCTAAATCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
 TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
 CCGTGTGGTGCATCATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTACTCTGCTTCG
 ACAAGAATAACCCAGCAACAACTGGTGAGCAGAGCAACACAGTCACGGCAGCCACATC
 AAGAAGTTTCACTTCTGCTGTCATGGCTCTGTCACTCAGCCTCTGTTTTCGTGATGTTTGGAC
 ACCCAACGCTCTGAGAAAACTTGTATAGACATCATCGGAGTGGACTTTGCCCTTTCGAGAAC
 TCTGTGTTGTTCTCTTTCGCGATCTTCTCCTTCTTCCAGTTTCAGTGCAGGTGAGGGCGCAT
 CTCACCGGTGCTATGACACTGAAGAAAACCTTCTGCTTGGCCCCAGTCTGTGCTGCG
 GATCATCGTCTCATGCCAGCCTCGTGGTCTACCTTACCTGGGGGTGCACGGTGCAGCCC
 TGGCGGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGTCGCCATCGCTGCG
 TGCTATGTCTACCGGAAGCAGAAAAAGAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA
 CTCTGCCATGACAGACATGCTCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAGG
 AGAATGAATAAGGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC
 GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTGGTTTTTGGTAAAT
 GAAAGAGGCGTTGATTTAAAGGTTTTCGTGTAATCTCTAGCATACTGGGTATGTCACACT
 GACGGGGGACCTAGTGAATGGTCTTACTGTTGCTATGTAAAAACAAACGAAACCACTGAC
 TTCATACCCCTGCCTCAGCAAAACCCAAAAGACAGCTGCCTCAGCGTTGACGTTGTGTCC
 TCCTCCCCTGGACAATCTCTCTTGGAAACCAAGGACTGCAGCTGTGCCATCGCGCTCGGT
 CACCTGTCACAGCAGGACACAGACTCTCCTGTCCCCCTTTCATCGCTCTTAAGAATCAACAGG
 TTAATACTCGGCTTCCTTTGATTGCTTCCCACTCATGCGCGTACAAGAGATGGAGCCC
 CGGTGGCCCTCTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG
 GAGGCGGGTGGCAGCGTGCAGGCCGGAGTCCCCGTTCACTGAGGAACGGAGACCTGTGAC
 CACAGCAGGCTGCAGATGGACAGAAATCTCCCGTAGAAAGGTTTGGTTTTGAAATGCCCCGGG
 GGCAGCAAACTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCTGATCTGTAGCAA
 GCTGTGAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTACAAAA
 GCGCATCTCCAGATTTCAGACCCCTGCCGATGACTTTTCTGAAAGGCTTGCCTTTCCCTCGC
 CTTTCTGAAAGTTCGATTTAGAGCGAGTCACATGAGGATCTTCACTTTGCAATTTAGTTT
 TACAGTGAATGAGCTTTAAGTCTCATCCAGCATTTCAATGCCAGGTTGCTGTAGGGTAAAC
 TTTTGAAGTAGATATATTACCTGGTCTGCTATCTTAGTCATAACTCTGCGGTACAGGTAA
 TTGAGAATGTATACCGTACTTCCCTCCACACCATACGATAAAGCAAGACATTTATAACG
 ATA CAGAGTCACTATGTGGTCTCCCTGAAATAACGCATTGCAAAATCCATGACAGTGCAGTA
 TATTTTCTAAGTTTGGAAAGCAGGTTTTCCTTTAAAAAATATAGACACGGTCTCACT
 AAATTGATTTAGTCAGAATTCTAGACTGAAAGAACCTAAACAAAAAATATTTTAAAGATA
 TAAATATATGCTGTATATGTATGTAATTTATTTAGGCTATAATACATTTCCATTTTCGC
 ATTTTCAATAAAATGCTCTAATACAAAAA

10017351.102401

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSIDLGYIINKLHHVDESV
GSKTRRAFLYLAAPPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLLIPILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQIRSRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNFTVAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFELCVVPLR
IFSFFPVPTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVHGATLGVGSL
AGFVGESTMVAIAACYVYRKQKKKMNESATEGEDSAMTDMPTTEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCACAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACTTCGTC

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FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAAACCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCTTTGCGGATTTTCT
CCTTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTACCCGGNGGNTGATGACANTGAAG
AAAACCTTTGTCCTTGCCCCCAGCTINTTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT
GGTCCTACCCTACCTGGGGGTGCACGGTGCACCCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCTACCTGGGGGTGCACGGTGAGAC

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2015. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 8

GCCCCGCGCCCGCGCCGGCGCCCGAAGCCGGGAGCCACCGCATGGGGGCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG
CTGCTGCCCCCGCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCAGTTCTTCTCTTCC
TGGGGGTGCTGGTGTCCATCATATTAGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCTCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCTTCTTCTTCT
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCGGGCTGCCATCCAG
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGG
AAGGCCGAGGAGTGCATTCCCGTGCTGGTACGACGGCCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTATGTACTACATGAGCCCGAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGCTCTGCTGACGGCCTCGGTAT
CACCTCTACACCATGTTTGTCACTGGTCAGCCCTATCCAGTATCCTGAAACAGAAATGCA
ACCCCATTTGGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGGAGCATTGTGGGCTCATCATCTTCTCCTGTGCACCTCTT
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGAGGTGGCAGCCTGTGAGGGCCGGGCC
TTTGACAACGAGCAGGACGGCGTCACTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT
GGCCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGTGAGACCCGGAAGA
TGATCAGCAGCTGGACCGCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC
TACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGGACTTCAGCTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCCCTCTCGGCTCGGTGACAGCCAACCT
GCCCTCTCCCCACACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCCTGAGCCGGGCTTCTAGTCGTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCCATCCCCCGCCACACCACAGGTGGAGCTGCCTCTTCTTCCCTCCTCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCTTGTCTCAGGCTCCACGGGAGCGGGG
CTGCTGGAGAGAGCGGGGAACCTCCACCAAGTGGGGCATCCGGCACTGAAGCCCTGGTGTT
CCTGGTCAGTCCCCAGGGGACCTGCCCCCTTCTGGAGTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAACAAAAA

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRIFTFFLFLGVLVSIIMLSPGVE
SOLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGVSFLFILIQLVLLIDFAHSW
NQRWLKGAECDRAWYAGLFFFTLLFYLLSIAAVALMPYYTEPSGCHEGKVFISINLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVITYSYSFFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVWKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 10

GAGCGAGGCCGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAGAAGGCCATGGAGGTGCCGCCACCGGC
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCATTTCCCCGAGCTTTTGTGCGCGAAGCTG
TGACTGCCGATTTCGGAAGTCTTGAGGAGCGTCAGAAGCGGCTTCCTACGTCCCAGAGCCC
TATTACCCGGAATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGG
TGTATGGGGGAATACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGTGCCACACGAGGCTT
CATTTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTGTGTGACTATATTTCAACACAG
TGAACACTAGTCTGAATGTATACCGAAATAAGATGCCTTAAGCCATTTTGTAAATGTCAGGA
GCTGTCACGGGAAGTCTTTTAGGATAAACGTAGGCCCTGCGTGCCCTGGTGGCTGGTGGCAT
AATGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCCTGCTGATGGCATTTCAGAAGTACGCTG
GTGAGACTGTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCACCTCCATGAGCTAAAACTGGA
GAGTGGAAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAAATTGAAAGTAGTTTACG
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACGTCTAAACCTTCCTAGAAAAC
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC
TGACAAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTTGCTTTTTCTTTCTT
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA
GCAGTAAATAAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

FIGURE 11

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAEIYHNRFDAVQSAH
RAATRGFIRYGWRWGWRVAVFVTIFNTVNTSLNVYRNKDALSHEFVIAGAVTGSFLRINVGRLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE
KIESSSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTG CCTATTTC CCGAGTTT TGTGCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATT CATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 15

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979
><subunit 1 of 1, 204 aa, 1 stop
><MW: 22147, pI: 8.37, NX(S/T): 3
MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLVFIQFSVSCACIALNQEQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL
TYRYRNQKDPANPSAFL
```

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTTNTGGAGGTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTAAACCCAAATGACACCTGTNTGGCTAGCTGTGTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAG

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FIGURE 17

AAATCCCAAATCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG
TTATGTCTTAGGAAATTGTGGTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
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FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCAGAGAAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

FIGURE 19

CAGTCA~~CCATGA~~AGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAACCTTCCACCTGATTGTGTCTTATGACTGGCTG
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCCTAACAGGGAATTCTCCATCACCGTGGTCAAAAGGCAGACAGCGGGCACTACCAC
TGCATGGCATCTTCCAGAGCCCTGGTCTGGGATCCAGAAACAGCATCTGTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCTGAGTTGTTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAACACAGAGCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAATGCTCCTGA
GGAGGCCCTTGGGCCTCTGCTCCGCGCCAAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG
CAGGATGTGAGAGTCTCCTCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTTCATCCATGATCTCACT
TAACCAACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGCTCTGCACATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTTTTGTAGAAATAATGTAGTTAGGTGAGTGTAAATAAATTT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAAATGTTGTGATTTAAAGAGAA
CTAATGGAAAGTGGAATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGGCCCCCAGAGGACA
TTGGGCAATGTTTGAGACATTTTGGTCATTATACTTGGGGGGTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCTTATAATGCACAG
GGCAGTACCCACAACGAAAAATAATCTGGCCCAAATGTGAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCGTCTCTTTAGTTCTAGTTTGTATCCCTCAAAAGCCATTATGTTGAATTCCTAATCCCC
AAGGTGATGGCATTAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTCGCCAAACACCG
ACTCTGTCTGTGCTTGTATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG
TTGTTTGTAGCCATA

FIGURE 20

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGLWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSGALGPFPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPOKSAAPGTAPEEAPGFLPPPPPTPSSSEDPGFSSPL
GMPDPHLYHQMGLLLKHMVDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

FIGURE 21

CCCACGCGTCCGCCCACGCGTCCGCCCACGGGTCCGCCCACGCGTCCGGGCCACCAGAAGTT
 TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
 ATCTTACTGGGCGTGCTACTCTCGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
 GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
 ACCCCTTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCT
 GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAAGTACCAGGGCCG
 CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTGGAGATGG
 ATGACCGGAGCCACTACAGTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
 AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCACAGTGACAAC
 TGGCAGCGGTTATGGCTTACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC
 GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCCAGGAACCCATC
 AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
 TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
 TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC
 TTGAAGCAACATCTACAGTGAAGCAGTCCCTGGGACTGGACCATGACATGGATGGCTACCT
 TGGAGAGACCAAGTGCTGGGGCCAGGAAAGGCTGCGCTGTCTTGGCCATCATCTCATCATCT
 CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCAA
 CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT
 CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGGGCAAGAGCCC
 AATCCTAAGGCCGAGGCGCTTCAAGGTCAGGACATAGCTGCCCTCCCTCTCTCAGGCACCTT
 CTGAGGTTGTTTTTGGCCCTCTGAACACAAAGGATAAATTAGATCCATCTGCCTCTCTGCTTCC
 AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
 AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
 TGCCAGAGAGGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT
 CCAGTGATGAGCCAACCTCCAGAACTTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA
 CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCCGCTGCTGGACACAGTTCC
 TCTGGATTATGAGTTCTTGCCACTGAGGGCAAAAGTGTCTGTAAAAAATGCCCAATTAGGC
 CAGGATCTGCTGACATAAATGCGCTAGTCAGTCTTGCCTTCTGCTAGGCCCTTCTCCCTGCT
 ACCTCTCTTCTGGATAGCCCAAAGTGTCCGCTACCAACACTGGAGCCGCTGGGAGTCACT
 GGCTTTGCCCTGGAAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
 GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
 CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA
 CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
 TTCTCTTTCTTCAAGGCCAGACAGCTTTAATTGAAATTTGTTATTTACAGGCCAGGGTTCA
 GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
 ATCATAACAGC

10017594.102401

FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVRGRS
DPVTIFLRDSSGDHIQQAKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRIQLQCQARGSPPIISYIWKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKVVVDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWTIDMDGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

FIGURE 23

GCGCCGGAGCCCATCTGCCCCAGGGGCACGGGGCGGGGGCCGGCTCCCGCCCCGGCACAT
GGCTGACGCCACCTCGCGCGACCCCGAGGCGCGCGCCAGCTCGCCCGAGGTCCGTCGGA
GGCGCCCGGCGCCCCGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCGCGTCCGGGGATC
GGGATGTCCTCCTCTCTCTCTCTGTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTGGCCCTGCCACCATCAACTGGGGC
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCAGTAATGAAGGGAAACCAAAAA
GTGGTGATCACTTACTCCAGTCGTCTATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG
AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCCTTGCAGATTGAACCTCTGAAGC
CCAGTGATGAGGGCCGGTACACTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
GTCATCTTAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCTCCCAAACTCTAGGATT
GACTACAACCACCTGGACGAGTTCTGCTGCAGAACTTACCATGTCTACTCTGGACTGTA
CCAGTGACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCAGTAACCTGTACAGT
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG
ATTTTCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCAGCCTCTGGTCTCTCTCCACTCGCTCCACAGCAAAAT
AGTGCTCAGCGCAGCGCAGCGGACACTGTCAACTGACGACAGCACCAGCCAGGCGTGGCCAC
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAGAAAGTCCACCATG
CTAATCTGACCAAAAGCAGAAACCAACCCAGCATGATCCCAAGCAGAGCAGGCTTCCAA
ACGGCTGGAATTACAATGGACTTGACTCCACCGCTTTCTAGGAGTCAGGCTCTTGGACTC
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA
GTGAGCATTGCACGGAACAGATTGAGATGAGCATTTTCTTATACAATAACCAAAACAGCAAA
AGGATGTAAGCTGATTCTCTGTAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG
AGGTGAATATACCTAAAACTTTAATGTGGGATATTTGTATCAGTGTCTTTGATTACAATTT
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCAATTTCTGCAAACTTATTGGATT
ATTAGTTATTCAGACAGTCAAGCAGAAACCCAGCCCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACCTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCAATAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCACTATTGTATTGAGGCCCAAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATGTGAAGAGCTTCCATCTTCATGATGTT
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGTGGATTTCCTCTCAAT
CAGATGCCCTAAGGACTTTCTGCTAGATATTTCTGGAAGGAGAAAAATACAACATGTCTATT
TATCAACGTCTTAGAAAGAAATTTCTTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATT
CCCAACATACCAATTATAGTCTCTCTTTCTGAGAAAAATGGAACCAAGATTGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTGCCAGGCACCTGTAGGAAAAATCCAGCAGGTGGAGGTTGCACTGAGCCGAGATTATGCC
ATTGCACTCCAGCCTGGGTGACAGAGCGGACTCCGCTCTC

1000 900 800 700 600 500 400 300 200 100 0

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

FIGURE 25

GTCGTTCCCTTTGCTCTCTCGCGCCAGTCTCTCTCTGCTTCTCTCTCAGCCGCTGTCTGGAGGAGCAACCGGA
 GACGCGGGCTGCAGTCTGCGGGCGGCTTCTCCCGGCTGGGCGGCTCTGCGGCTGGGCGAGTCTGAGCGCCCTTAG
 AGCCTCCCTTGCAGCTCTCTCTCTGCGCGCCGAGCAGTGCACATGGGGTGTGGAGGCTAGATGGGCTCCCG
 GCCCGGAGGGCGGCGTGGATGCGGCGCTGGGCAGAAAGCAGCGCGGATTCACGCTGCGCCGCGCGCCCGGGCG
 CCCTCTGCGAGTCCCGGTTTCAGCCTATGGGAGCTCTCCGAGCAGCAGCACCGCCCTCGCCTCTCTGACCGCCATC
 GCOCGCCGAGCCACAGCCACGATGATCGCGGCTCCCTTCTCTGCTTGGATCTCTTAGACACCAACAGCAGCTCAG
 CCAGAACAGAAAGCCCTCGAATCTCATTTGGCACATACCGCCAGTGTGACCGTGCACCGGCGAGGGTCTAACTGT
 GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTTGACCAACAGCAAGCTCTGCGCGTCTGAGCAGTGTGCCCT
 GTGGGACCTTTACCAAGGCTAGGAATGGCATAGAGAAATGCCATGCTAGTGCAGCCATGCCCATGGCCAAATG
 ATTGAGAAATACCTTGTCTGCTGCTGACTGACCGAGAAATGCACTGCCCACTGGCATGTTCAGTCTTAACGCT
 ACTTGTCGCCCCCATCGTGTGTGCTCTGTGGGTGTGGGTGTGGGGAAGGGAAGGAGCAGAGACTGAGGATGTGGCG
 TGTAAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAGCATACACAGACTGT
 CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGGAACCAAGGAGACAGACAACGCTGTGTGGCACTCTCCGCTCTTC
 TCCAGTCCACCTCACCTTCCCCTGGCAGAGCATCTTTCCACGCGCTTAGCACAATGGAACCCATGAAGTCCCT
 TCCTCCACTTATGTTCCCAAGGCTAGACTCAACAGAATCCAACCTTCTGCTCTGTGAGCCAAAGGTACTG
 AGTAGCATCCAGGAAGGGACAGTCCCTGACACACAAGCTCAGCAAGGGGGAAGGAAGCAGTGAACAAGACCCCTC
 CCAAACTTCAGGTAGTCAACCAACAGCAAGGCCCCCAACACAGACATCTGGAAGCTGTGCGCTCCATGAGG
 GGCATGGGGCGAGAAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCTTAGACAGAACCTTACACAAG
 CATTTTGACATCAATGAGCAATTGCCCTGGATGATTTGTGCTTTTCTGCTGCTGGTGTGTTGGTGTGTTGGTG
 TGCAGTATCCGGAAGCTCGAGGACTCTGAAAGGGGGCCCCGAGGATCCAGTGCCATTTGTGGAAGAGGCA
 GGGCTGAAGAAATCCATGATCTCAACCCAGAACCGGGAGAAATGGATCTACTGCAATGGCCATGGTATCGAT
 ATCCTGAAGCTGTAGCAGCCCAAGTGGGAAGCCATGGAAGATATCTATCAGTTTCTTGTCAATGCCAGTGAG
 AGGGAGGTTGTGCTTTCTCCAATGGGTACACAGCGGACCAAGAGCGGGCTACGAGCTCTGACGACTGGACC
 ATCCGGGGCCCCGAGGCCAGCTCTGCCAGCTTAATAGCGCCTGCGCCAGCACCGGAGAACGATGTTGTGGAG
 AAGATTCTGTGGCTGATGGAAGACACCCAGCTGGAAACTGACAACTGCTCCCGATGAGCCAGCCAGCCCG
 CTTAGCCCGAGCCCCATCCCGAGCCCAACGCGAACTTGAGAAATTCGCTCTCTGACGGTGGAGCCTTCCCCA
 CAGGACAAGAACAGGGCTTCTTGTGGATGAGTCGGAGCCCTTCTCCGCTGTGACTCTATCATCCAGCGGCTCC
 TCGCGCTGAGCAGGAACGGTTCTCTTATACCAAGAAAGAAAGGACACAGTGTGGCGGACATGCGCTGGAC
 CCCTGTGACTTGCAGCTATCTTTGATGACATGCTCTCACTTTCTAAATCTGAGGAGCTCGGGTGTGATGAAGAG
 ATTCCCAGGCTGAGGACAAACTAGACCGGCTATTCTGAAATATTGAGTCAAGAGCCAGGAAGCCAGCCAGAGC
 CTCTGGACTGTGTTATAGCCATCTTCTGACCTGCTGAGAACATAGGATCTGCACTTTGGAATATGACTCA
 ATTAGTGGCAGGTGGTTTCTTAAATTTCTCTGTGTTCTGATTTTGTGTTGGGGTGTGTGTGTTGTTGT
 GTGTGTGTGTGTGTGTGTGTGTGTGTGTTTAAACAGAAATAGGCCAGTGTCTGAGTCTTTCTCTCTCTCTC
 TCTCTCTCTTTTTTTAAATAACTCTCTGGGAAGTTGGTTTATAGGCCCTTTGCCAGGTGTAACCTGTGTGAA
 ATACCCACCATCAAGGTTTTTTAAAGTCCATATTTCTCCATTTTGCCCTCTTATGATTTTCAAGATTATCTGT
 TGCACCTTTAAATTTACTTAACTTACATATAATGCAAGTGTGACTTTTCCACACATCGGATTGTGAGGCTCTTAA
 TTCTTAAAGATATAAGTGCATCTGTGAATCTTAAAGCAGTCTTATGTCTCTTAACTTCAACCTACTTTT
 AAAAACAATAATATTACTATTTTATTTATTTGTTGCTTTATAAATTTCTTAAAGATTAGAAAAATTTAAGA
 CCCCATTGAGTTACTGTATGCAATCAACTTTGAGTTATCTTTTAAATATGTCTGTATAGTTCATATTCTATG
 CTGAACTTGACCACTATTTGCTGATTGTATGTTTTCACCTGGACACCGTGTAGAATCTTGTATTTCTGTATC
 TCTTCTTATCTAATATGCTCTGGGCTGGAGAAATGAATCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
 GACACTGGGCGCAACCAAGAACTTGAACCTTCACTTTTAGGATTTGAGCTGTGTTGGAAACACATGCTGCACTTT
 GGAAGTCAAAATCAAGTGGCAGTGGCGCCCTTCCATAGAGAAATTTGCCAGCTTTGCTTTAAAGATGTCTTG
 TTTTTTATACACATATCAATAGGTCCAATCTGCTCTCAAGGCTTGGCTGGGTGATTCCTTCAACAATT
 ACTTTAAATTTAAATGGCTGCACTGTAAGAACCTTGTCTGATATATTGCAACATGCTGCCATTTTCAAAATG
 TACCTTCTAATGCTGATTTGCCAGGTTTCCAATGCAAGGTGCGTGGACTCCCTTGTGTGGTGGGGTGTGGTGG
 GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTATTATAAACAATTAGGTGTTGTGTA
 AAAAAAAA

10077001-102443

FIGURE 26

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSFSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFFTRHENGIEKCHDCSQPCPWPMIEKLPCA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWVRKKGTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKKHFDINEHLPWMIVLFLLLVLVVI VVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKLALPMSPSPLSPSPISPNAKLENSALLTVEFSPQDKNKGFFVDESEPLL
RCDSTSSGSSALSRRNGSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEEIGVKSQEASQTL LDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

[illegible]

ATGGGAAGCCAGTAAACTGTGGCCCTACTATCTCTTCGTTGGTGCCATCTCATCTTTTGGGA
 CTGGGAATAATTAGAGTAGAGGTGGAGGCGGAGCCGGATGCTCAGAGGTCCTGAATAATGCAC
 CATGGGGGAAATGATATCGCTCGCTGTGTTGAAGCCCTTCTCATCTCCGATCGCTTTTGGCC
 TTGATGATTTGAAATAAGTCTGTGTTCACAGACATCAGATGCTGTGTCTGCACAGATCCCTG
 TCACTGTGCTGCATTTGAAGTTTTTCGAATCATGTCATTTGGGATCATTGTCATGTAATTAGC
 ACTGGCCATTGSGTCTGGGCATCCACTTTCGACTGCTCAGGGAAGTACAGATGTGCTCATCCT
 TTAAGTGATCGAGCTGATATCTCGATGTGACGAGGATCTCGGATGTCAAAGACGGGGAGGA
 GAGTACCGCTGTGTCCGGTGGGTGGTCAGAAATGCGCTGCTCCAGGTGTTACAGACTGCTTC
 GTGGAAGACCATGTGCTCCGATGACTTGAAGGGTCACTACGCAAAATGTTGCTGTGCCCAAC
 GGGGTTTCCCAAGCTATGTGAGTTCAGATAAACCCTCAGAGTGAGCTCGCTGGAGGGGCGAGTTC
 CGGGAGGAGTTTGTGTCCATCGATCACTCTTGCCAGATGACAAGGTGACTGTCATTACCACT
 CTAGTATATGTGAGGGAGGAGTGTGCCTCTGCGCCACGTGGTATCTTACCTGTCAAGTGCACAGCCT
 GTGTGTCATAGAAGGGGCTACAGCTACGCACTGTGGGTGGAAGAACATGTCCTTGTCTCGCAG
 TGCCCTTGGCAGGCGAGCTCTCAGTCTCAGGGCTACCACCTGTGCGGGGGCTCTGTATCAC
 GCCCCCTGGGATCATCACTGCTGCACACTGTGTTTATGACTGTACTCCCCAAGCTATGGA
 CCATCCAGGTGGGTCTAGTTTCCCTGTGTGGACAATCAGCCCCATCCCATCTGGTGGAGAGA
 ATTGTCTACCAACAGCAAGTACAAGGCCAAGAGGCTGGGCAATGACATCACTGCGCTTATGAAGCT
 GCGCGGGGCCACTCAGTTCAATGAATGATCCAGCCTGTGTGCTGCCCACTCTGAAGAGA
 ACTTCCCCGATGAAAAGGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAG
 CCTCCCTCTGTCTGTAACACCGCGGCCGTCCCTTTGATTTCCAAACAAAGATCTGCAACCAACAG
 GGACGTGTACGTTGCAATCATCTCCCCCTCATGCTGCGCGGGCTACCTGACGGGTGGCG
 TGGACAGCTGCGCAGGGGGACAGCGGGGGCCCCGTGGTGTGTCAAGAGAGGAGGCTGTGAAGT
 TTAGTGGAGCGCACAGCTTTTGGCATCGCTCGCGCAGAGGTGAACAAGCGTGGGTGTACAC
 CCGTGTCACTCTCTTCTGGACTGGATCACGACGAGATGGAGAGAGACCTAAAAACCTGGA
 GAGGAAGGGGACAGGATAGCCACTGAGTTCTTGAGGTGATGAAGACGCGCGATCTCCCTCT
 GGACTCCGCTGTAAAGATCTGCACACGAGCAGACACCTTGAGAGCTGTGAGTTCGGCCACCA
 GTAGCAGGCCCCGAAAAGAGGCACCTTCCATCTGATTCAGCACCTGCTTCAAGCTGTCTTTT
 GTTTTGTGTTTGTGAGGTGGAGTCTCGCTCTGTTTGCCCAAGCTGGAGTGCAGTGGCGAAA
 TCCTGTCTCACTGACGCTCGCTTCTCCCTGGTTCAAGGATTCCTGTGCTCACTCTCCCA
 GTAGCTGGGACACAGTGTGCCCGCCACCACTCAACCAACTAAATTTTGTATTTTATGAGAGAC
 AGGCTTTCACCATGTTGGCAGGCTGCTCTCAAAACCCTGACTCAATGATGTGCTGCTCTT
 CAGCTCTCCACAGTGTCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCACGCTCCTTTC
 TGATCTTCACTAAGAACAAAAGAGCAGCAACTTGAAGGGCGAGTTTCCCATCTGTTCCAT
 CTGTTTCTCTCAAGGGTCTTGCAAAATTTCTGCAGAGATAAGCAGTTATGTGACCTCAGT
 TGCAAAAGCCACACAGCCACTCTCAGAAAAGACGACCCAGCCAGGTCAGAAAGTGCAGTCT
 ACTGCACGTTTTCATCTCTAGGGACAGCAACCAACCCAGTTTCTACTTCCAAGACTTAT
 TTTCCATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCATATTTTCATGATTTCCT
 TGTAGATCTTTGGTGTGTACGCTATATTGTCTCTTGATTCCAAATAATGTTTCTCTCCCT
 CATGCTCTGGCGTGTCTGCGTGAAGTGTGAGTGAAGTCAAAATCATCACTGAAA

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVQLQVFTAAS
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIDHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIIITAAHCVDLYLPKSWTIQVGLVSLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSWGATEDGGDASPVLNHAAVPLISNKICNHR
DVGGGIISPSMLCAGYLTGGVSDSCQGDGGPLVCQERRLWKLVGATSFSGIGCAEVNKPVGVT
RVTSTFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

FIGURE 29

CCCACGCGTCCGTCTTAGTCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGCGTCAAGGCTGGCTTGT
 GCCAGAACGGCGCGCGCGCGCACGACGACACACACGCGGGGGAACCTTTTTTAAAGATGAAAGGCTAGAAGAG
 GCTCAGCGCGCGCGCGCGCGCTGCGCGGAGGCTCGGAGCTGACTCGCCGAGGACAGAAATTCCTCCGGTCGCGA
 CGCCCGGCGCGGCTCGCGCGCGCGCTGCGGATGGTGCGAGCGCTCGCCGCGCGGCGCGGCTGCGACAGG
 GCGCGCGACAGTGCAGCGCGCGCGCTGCGCGGTGTCGCCGCGCGCGCGCTCTGCTCGCTCGCTGGCGCGTCT
 GCTCGCGCGCTGCGAGCGCGCGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTTGTGAGTGCTCTGT
 TCGAGTGTGGGACCTCTGATCCAGTGGAAGAGCTTCGACTCCAAGAATCATCCAGAGTGCTGAATATTGCACT
 ACACCGGGAAGACAAAGAACTGATCAATAATCTGGAAGAAATGAAGGTCTCATTTGCCAGCAGTTTCAACGGAAC
 CCATATCTGCAAGAGCGGTACTGATGTCTCCCTCGCTCGAAATTAACCGGTCACGTGTTACTACCAATGGACATGT
 ACGGGGATATCTGATTTACGACAGTCAGTCTCAGCACGCTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAGATGA
 AAGCTATGTTTATAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCAGCGAAGAGCTGAAAAGGCT
 CCGGGGATCATGTGGATCACATCAACAACACCAAACTCGCTGCAAGAAATGTGTTTCCACCAACCTCTCAGAC
 ATGGGCAAGAGGCAATAAAGAGAGACCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCTGGGCAGACCAACG
 AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGAAAGTTAAGCAGCGATTAAATAGAGATTGCTAATCACGTTGACAA
 GTTTTACAGACCACTGAACATTTCGGATCGTGTGTGGTAGGCGTGGAAGTTGGAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCACTCACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA
 TGACAAATGCGCAGCTTGTGAGTGGGGTTTATTTCCAAGGGACCAACCTCGGCATGGCCCAATCATGAGCATGTG
 CACGGCAGACAGCTGTGGGGGAATTTGTCATGGACCATTCAGACAAATCCCTTGGTGACGGCGTGACCTGGCACA
 TGAGCTGGGCCCAAAATTCGGGATGAATCATGACACACTGGACGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCATGGTGTTCAGCAGTTGACAGCAGGAAGGACTT
 GGAGACCGAGCTTGAGAAAGGAATGGGGGTGTGCTGTTTAACTTGGCGGAAGTCAGGGAGTCTTTCGGGGGCCA
 GAAGTGTGGGAACAGATTTGTGGAAGAAGGAGGAGTGTGACTGTGGGAGGACAGAGGAATGTATGAATCGCTG
 CTGCAATGCCACCACTGTACCTGAAAGCGGACGCTGTGTGCGCAGATGGGCTGTGCTGTGAAGATCGGAGAT
 GAAGCTCGCAGGAACAGCGTGCAGGAGCTCCAGCAACTCTGTGACCTCCAGGATCTTCGACAGGGGCGAGCCC
 TCACTGCCCAATCATGTGTACTGTGCACATGGGCACCTCATGTGAGATGTGAGCGGCTACTGCTCAATGGCAT
 CTGCCCACTCACGACGAGCTGTGTGACGCTCTGGGACCAAGTGCTAAACCTGCCCTTGGGATCTGCTTTGA
 GAGAGTCAATTTGTCAGGTGATCTTATGGCACTGTGGCAAGTCTCGAAGAGTPTCTTGTGCAATGGAGAT
 GAGAGATGCTAAATGTGGAAAAATCCAGTGTCAGGAGGTTGCCAGCGGCGAGTCATGTTGATCAAACTGCCCTTC
 CATAGAAACAAACACTCCCTCTGCAGCAAGGAGGCGGATTTCTGTGCGGGGACCAAGCTTGTGCGCATGAC
 CATGCCGACCCAGGCTGTGCTTGCAGGCAAAAGTGTGCAGATGCAAAATCTGCTGAATCGTCAATGTCA
 AATATTAGTGTCTTTGGGGTTCCACAGTTGCAATGCCAGCGCAGAGGGGTGTGCAACACAGGAGAA
 CTGCCACTGCGAGGCGCACTGGGCACTCCCTTCTGTGCAAGTTTGGCTTTGGAGGAAGCAAGACAGCGCGCC
 CATCCGCGACAGCAAGCAAGGACGAGAGCTGCGAGTCCACAGGAGGCGCGCGCGGCGCAGGAGCCCGTGGG
 ATGCGAGGAGCATGCTCTACTGCTCAGTGACACTCATGAGCCCTCGAGCCCTCCCATGACATGGAGACCGT
 CTGCTCAGAGGAGGTGAGCGTCCCCAAGGCTCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
 TCCATGACACACAGACCAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCTTACCAGGCGAGTCTGACAGAA
 CAGTGCAGGAGAGGGCAGCGACTTCTGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGTGCTCTGAG
 AGAGTAGCAGTTTACCATCTGGCAGGCGCCAGCCCTGACGCAAGGAGGAAGAGGACTCAAAAGCTTGGCCTTTC
 ACTGAGCCTCCACAGCAGTGGGGGGAAGCAAGGTTGGGCCAGTGTCCCTTTCCCAAGTGACACCTCAGCCT
 TGGCAGCCCTGATGACTGTGTTCTGTGCTGCACTTAATGCTCTGATATGGCTTTTAGCATTTATTTATATGAAAT
 AGCAGGGTTTATGTTTAAATTTATCAGAGACCTTGCCACCAATTCATCTCCATCCAAGCAAACTGAATGGCAA
 TGAGAAACAACTGGAGAGAGGTTAGGAGAAAGGGCGGTGAATCTGCTGTGGACATGCGTGACAGCAGC
 AGTACTCAGGTTTGAAGGTTTGCAGAAAGCCAGGGAACCAACAGAGTCAACAACCTTCAATTAACAGTAGAAGA
 TGTAAAAGTAGAAACAAATGTAGAGCCTAACTCAATCCCGTGGCCATTAATGCTCAATAAATAGAGTGCAATTT
 GAAT

1007031.102401

FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTVDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLPAPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPPSQTWARRHKRETLKATKYVELVIADNREFQRQGDLEKVKQRLIEIANHVDKF
YRPLNIRIVLVGVEVWMDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGI VMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPPMVFSSCSRKDLETSLKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDCGEPEECMNRCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSNSNCDLPEFCTGAS
PHCPANVYLHDGHSCQDVGDCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN
CGKVSXSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLQGGGRI LCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRQCQNI SVFGVHECAMQCHGRGVCCNRRKNCHCEAHWAPP
FCDKFGFGGSTDGSPIRQAEARQEAAESNRERGGQGEVPVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

FIGURE 31

TCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTTTCAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAAATAGCAGGGTTT
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

1007331-02401

FIGURE 32

CATCCTGCAACATGGTGAAACCAACGCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTACCCTGTTAGCCAGGATTTGTCTCAATCTGACCTCATGATCTGCCCGCTCGGCCCTCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAACTTTTAAAGAGTTAAT
GAAACCATACTTTTACATTTTAAATGACAGGAAAAATGCTCACAATAATTGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAATACATGTATATGTACTATATGAAAAATA
TACCAATATCAATAATACTTATCTCTGGGTA AAAACCTCTTCTCATACCTGTGCTAACAA
CTTTTAACAAAAAAATTTGCATCACTTTTAAAGAAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA
AACAAAGTACTTTGTCTGGATGTAGGAGGAAAGGAGTGATGTCAGTGCCATTATGATGCCCC
TTGAATATAAGACCCCTACTTGCTATCTCCCTGCACCGCAGGAGCCACCATCTCTCCAGC
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCTTACCGTGCAGGTTTCTTCATTTGTT
CCTTTAACCAAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAAAGTGCCCT
ACAGCCTACAGCCGGTCTCCTTGTTGCTTGCTTGCCCTTCTACATCTCTACCATTAAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT
AGAAGTTCAATGTGGCAAGGAAAAAACAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGCCCTAGGCCGGGATCACCTG
AGGTGAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATGACTGGGCGTGGTGGTGAAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCTCTCAAAAAAAAAAAGCCAAGTGCAAGTGGCT
CACGCCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA
AGACCCTCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAATAGCGTGAA
CTCAGGAGGCGGAGCTTGCACTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGCAGC
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

FIGURE 33

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309
><subunit 1 of 1, 67 aa, 1 stop
><MW: 6981, pI: 7.47, NX(S/T): 0
MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL
LHLYH
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Signal peptide:

amino acids 15-27

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Critique

[illegible]

FIGURE 35

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAADGPPAADGEDGQDPHS
KHLYTADMFTTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNMEDAKVYVAKVDCTAH
SDVCSAQGVRGYPTLKLFKPGQEAVKYQGPRDFQTLNWLQTLNEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT
QHVELCSGNQVRGYPTLLWFRDGGKVDQYKGKRDLESLEHYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLFRGGKVVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:

amino acids 1-32

FIGURE 36

CTTTCTGAGGAACCAAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT
GTCTGTGATTGTGGAAGATACCGGAAATTTGTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCTGCAGGATTCGG
GGTGGAAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGTGACTATGTTGC
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTGTCTGTGAGTTTCATCAAGAAGAAAAAGTAACTTCCGTCATCCT
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAA

FIGURE 37

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASLLRRNQFILLVLFLQLQISLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEGEEG
KHGKVGVRMGPKGIKGBLGDMDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRY
RKFBVGQLDISIARLKTSMKFVKVNIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQYNSNWNNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:

amino acids 1-25

FIGURE 38

GGTTCATCGATTGCAATTGCGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGGCTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT
GCCAGCGTCGCTGCTCCTCGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT
CGGAAGGGAGGATCAGGGATGTTTGCAGACGGCTGGAACAGACGGTGCCGATAGAGGAAGC
GGGTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTGTACCCTGCTGCTGCTGA
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGGCTTTGCGGTGCGAGCT
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG
TCCCAGGGGGGCTGACAGCTTGGCTTGGCCCTCGCGCCTCGCGGAAGTGGCCAGCAGCGCCGCGC
ACACCTTTTCTATTACGGCTCGCGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCCTTCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGCGCGCGACAG
CGCGAGGGGAGCGCTGGAGAAGGCGAGCGGCGAGCGCCGGGAGCCGGAGATCAGCGCGCG
GAAGCGCGCGGAGTTTCCGCGAGGGGACGGTGCCCGCAGAGGTGGAGGAGCGCCGCCCT
CTGTACACCTGGAGCACTGTGGCGCTGCTCTCCCGCTGGCCAGAGTTTCTGTGGCTCTG
GTTGGGCTGGCCAAGGCCGGCTGCGCACTGCTTTGTGCCACCGCCTGCGCGGGGCC
CCCTGCTGCACTGCTCCCGAGCTGCGGCGCGCGCGCTGGTGTGGCGCAGAGTTTCTG
GAGTCCCTGGAGCGGACCTGCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAAG
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACAGTGCCTGTACATCTTC
ACCTCTGGCACCCAGGGCTCCCCAAGGCTGCTCGGATCAGTCACTGAAGATCCTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCAITGGGGCCACAGT
GTGCTGAAATCCAAGTTCTCGGCTGGTCAATTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACCAGCCCCGAGCAGGGCAG
AACGTGGCCATAAAGGTCGCGTGGCAGTGGGCGAGCGGGCTGCGCCAGATACCTGGAGCGT
TTTGTGCGGCGCTTCGGGCCCTGCAAGTGTGGAGACATATGGAAGTGCAGAGGGCAACGT
GGCCACCATCACTACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGCTTTACAAGC
ATATCTTCCCCCTCTCCTTGATTGCTATGATGTCAACACAGGAGAGCCAAITCGGGACCCC
CAGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGTGGTGGCCCCGGTAAGCA
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGAAGTTGCTAAAGG
ATGTCTTCCGGCTGGGGATGTTTTCTTCAACACTGGGACCTGCTGGTGTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGAGAAATGTGGC
CACAAACGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGCGATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CAGCTTTGGACCTTATGCACTCTACACCCAGTGTCTGAGAACTTGCCACCTTATGCCCC
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAACAGCAGAAAG
TTCGGATGGCAAAATGAGGGCTTCGACCCAGCACCCTGTCTGACCCACTGTACGTTCTGGAC
GAGGCTGTAGGTGCTTACCTGCCCTCACAACTGCCCCGATACAGCGCCCTCTGGCAGGAAA
CCTTCGAATCTGAGAACTTCCACACTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGG
CCGTGTCAGGTGTACTGGGCTGTGAGGATCTTTCTATACCAGAACTGCGGTCACTATTTT
GTAATAATGTGGCTGGAGCTGTATCCAGCTGTCTGTGACCTAAAAAATAAAAAA
AAAAAAGGGGCGCGCACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC
TTGGCCGCATGGCCCACTTGTATTGTCAG

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLPLLLLLP
LLKLHLWPQLRWLPADLAFAVRALCCKRALRARALAAAAADPEGPEGCCSLAWRLAELAQQ
RAAHTFLIHGSRFFSYSEAERESNRARAFLRALGWDWGPDDGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKIQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFYIIGELCRYLVNQP
SKAERGHKVRVLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW
LYKHIFPFSILIRYDVTGTGEPIRDPOGHCMATSPGEPGLLVAPVMSQQSFPLGYAGGPELAQGGK
LLKDVFRPGDVFFNTGDLVLCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site

starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

ATCTTTGGGTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGTGCCAACTCACTCTTCTTCTTCTACACTCTTGGACAATGGACACTGCCACAAAACCTACCGGTTTTCTATGAGAAGAGAGCAGTAATGCAACTTCGCTCCCTTTTGTGTTTCCAAAGAGTAGCGGGTGCCAGACTGAAGCTCTTCTCTTTCTTTCAGCTATCTGTGGGGACCTGTTTATTCTAGAGAGAAATCTTACTCAAATTTTCTGACAGAGAGATTTCTTCACTTCATTGCTTTTATGCTGCAGAAAGTAAAGGAATCTCAGCTGTGACAGGGTTTTTTTTTTTCTAAATTTAAAT

FIGURE 41

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKA RSCGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELL ENAEKSLN DMF
VRTYGMLYMQNSEVFQDLFTELKRYYTGGNVNLEMLNDFWARLLERMFQLINPQYHFS EDY
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSP TPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGP FNIES
VMDPIDVKISEAIMNMQENSMQVS AKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGH SKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMD DVCPTFEFEVTT EAPAVDPDRREV DSSAAQRGHSLLSWSLTCIVLALQRLCR
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Signal peptide:

amino acids 1-23

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTTCGACGCGCTTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGGGACCGGCCGCGGGG
TAGGGACCCGGCTTTGGCTTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGCGTTCTTCTCACTTCGCGCGCTGGTGTGTCGGGGAGATTCGGCAAACGCGCTAGG
AAAGGACTGGGGAAAATAGCCCTGGGAAAAGTGGAGAAGGTGATCAGGAGCGCGGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGSAGCGCTCCACTTCGACAGTTCTTTCAGAGTGTGGGGACCGCAGGACAGACGGCCGA
TCCGCGCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCAACGTCGAGGGCGCTCTGGCCACGA
AAAGTTCCTGTCTCACTGTGATTCTCAATTCTTGTCTGGTTTCTTCTCCAGAGAACTTTGGGGTGGAGATATTA
ACTTTTTCTTTTTTTTTTTTTCTTGGTGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAAAGTGAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTTCGAGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGTTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCGTCTGTTGGGTGCATG
TGTGCGCCGCGACGCGCGCGGGCGCGTGGTTCTCGCGGTGGAGTCTCACCTGGGACCTGAGTGAATGGTCCCCA
GGGGCTGTGCGGGGCATCCGCTCGCTTCTCCACAGGCTGTGTCTGTCTGCTGGAAGATGCTAGCAATGGGG
CGCTGGCAGGATTCTGGATCTCTGCGCTCTCACTTATGTTACCTGTCTGGGGCCAGGCGCTTAGAAGAGGAGG
AAGAGGGGCGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCACGACAACTTCACCTCCAGCGCCCATCTCA
TTTTTCATCTAGCGGATGATCAGGGATTAGAGATGTGGGTTACCAACGGATCTGAGATTAAACACCTACTCTTG
ACAAGCTCGCTGCGGAGGAGTTAACTGGAGAATACTATGTCCAGCCTATTTCGACACCATCCAGGAGTCAGT
TTATTACTGGAAGTATCAGATACACCCGGACTTCAACATTCTATCATAAGACCTACCCAAACCACTGTTTAC
CTCTGGACAATGCCACCTACCTCAGAACTGAAGGAGGTGGGATTAACACGCATATGGTTCGGAATGGCAGT
TGGGTTTTAACAGAAAAGAAATGCATGCCACAGAGAGGATTGATACCTTTTTTGGTTCCTTTTGGGAAGTG
GGGATTACTATACATACCAAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAGAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAACTTTAGCTTCCATA
ACCCCAACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTCATTACCACCTGCAAGCTCTCGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTCTCTGTAGATGAAGCAA
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAAACACAGCATTATCATTTACTCTTCAGATAATG
GTGGCCAGCCTACCGCAGGAGGGAGTAACTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTTGTCACATCACTG
ACTGTTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCAATCAATTGACCCCTATACACCAAGGC
AAAAAATGGCTCTCGGCAGCAGGCTATGGGATCTGGAACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
GAAATTGCTTACAGGAAATCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG
GTGGCACAATGAACGGATCACCTTGTCACTGGCAAAGGTATGGCTTTTCAACATCACAGCCGACCCATATGA
GAGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAGCTCTCAGGAGGCTCTCACAGTTCAACAAAAAC
TGCACTGCGCGTCAGGTATCCCCCAAAGACCCAGAAGTAACCTTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAGAGGAAACCAAGAAAAGAAAGCAAGCAAAAACTAGGCTGAGAAAAGCAAAAGAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAACACAGCAAAATTTGGCTCGATAATATCGTGGCCTAAGCGTCA
GGCTGTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAACACTGCTCTGCTCAGTG
CCAAGTGCTACTCTTGCAAGCCCACTTAGAGAGAGTGGAGATGTTTATTTCTCTGCTCTTTAGAAAAACGTG
GTGAGTCTGAGTTTCCACTGCTGTGCTTCACTGCACTGACCAAAACACTGCTTTGAATTATAGGAGGAGAACATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAACCACTACCTTTGATGAATTAAC

1007667-102400

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEGALLAQA
GEKLEPSTTSTSQPHLIFILADDQGFQFRDVGYPHGSEIKTPTLDKLAAEGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMVGKWHLGFNKKEC
MPTRRGFDTFFGSLLGSGDYIYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA
LKTYGYFNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSFRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECTGNCLQEILATATGSPLSLSATWDRGTGTMNGSPCQLAKVYGFSS
TSQPTHMRGWTYLTGIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGCGGGCGGC
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCTCTGGGTGGCAG
GTGGTTTTCGGGAACGCGGCGCAGTGAAGGCATCACGGGTGTTAGCATCGGCACGTCAAGCCT
GGGCTCTGTCACTATGGAACTAAACTGGCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAACAAAT
GCAGATGCTTTCCAGGATACACCGGAAAACTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCCGCCATGCCAACACAGATGTGTGAATACACCGGAAGCTCAAGTGTCTTTGCTT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAATCTTAGGACATGTGCCATGATAA
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCCGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGTCA
TTGGTTTCGAACTGCAATATATCATGTGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGACGCCACCATGCCAATTGCTTCAATACCAAGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCTGAAAATTCTG
TGAAGGAAGTCTCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCAAAAATTAAAAATGTTACCCAGAACCCACAGGACTCC
TACCCCTAAGGTGAACCTTGACGCGCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAAC
CTCATGGAGGTAAGAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT
AAGGTGAATGAAGCAGGTGAATTCGGCTGATTCTGGTCCAAAGGAAAGCGTAACTTCCAA
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGTCTCAATCATGGGATCTGTGACT
GGAAACAGGATAGAGAAGATGATTTTGAATGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCAAGAAAGACATTTGGCCGATTGAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCGGGAACTTCGAGTGTGTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAGTTGTATCAAGGAATGATGC
TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGCGCAAAATCGCAGTGG
ATGGCGTCTTGCTGTTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTTGACTTTGTATGTCACTTCCCTGGTTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTGAATTTACTAGCTGAAAAATTTGAATGTACCAACAGAAATATTATG
TAAGATGCTTTTCTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCAATTTCTGAATCTTTCCNCAATATATTATAAAATNNGGAAANGTCAGTTTATCTC
CCCTCTCNATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA
GAAAAATAGAAAAAAGACAGAGAAATGTTTAACTGTTTGACTCTTATGATCTTTCTTGA
AACTATGACATCAAGATAGACTTTTGCTTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC
TTGTATATTAAATTCCTTGTAAATAATA

1007337-124404

FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNNKRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPPK
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGACAGCTGCTG
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACACGCCCC
AGAATGGGAGCTGACTGATAATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT
GAGCTGGAAGGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAAGATATACT
TGTTTTGCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCAGCGTTCTCTGTGTC
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACACTTAGGGACGGGTGTC
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCTTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTGAAAAGAAGTTTGGATCTCAGAACAACCTTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

FIGURE 47

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343
><subunit 1 of 1, 289 aa, 1 stop
><MW: 32268, pI: 9.21, NX(S/T): 0
M V V V T G A S S G I G E E L A Y Q L S K L G V S L V L S A R R V H E L E R V K R R C L E N G L K E K D I L V L P L D L
T D T G S H E A A T K A V L Q E F G R I D I L V N N G G M S Q R S L C M D T S L D V Y R K L I E L N Y L G T V S L T K C V L
P H M I E R K Q G K I V T V N S I L G I I S V P L S I G Y C A S K H A L R G F F N G L R T E L A T Y P G I I V S N I C P G P
V Q S N I V E N S L A G E V T K T I G N N G D Q S H K M T T S R C V R L M L I S M A N D L K E V W I S E Q P F L L V T Y L W
Q Y M P T W A W W I T N K M G K K R I E N F K S G V D A D S S Y F K I F K T K H D

Important Features:

Signal Peptide:

amino acids 1-31

Transmembrane domain:

amino acids 136-157

Tyrosine kinase phosphorylation site.

106-113 and 107-114

Homologous region to Short-chain alcohol dehydrogenase

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTGCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCCG
 TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCGGTGCGGACACGCTGGGCCCTGTGCC
 TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT
 GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCCTAGGCCCTCA
 ACCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCCTGTG
 GACAGCGTGGGCCCGGCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC
 CTGGGTCTCCTACTGCTGCCCACTGCTTTGAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
 CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCAGTTGCCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
 GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCGAGCCCGCCATCGCTTCC
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGAC
 CTACGCAATCTGCGCTGCGTCTCATCAGTCGCCCCACATGTAAGTGTATCTACAACAGCT
 GCACCAGCGACACCTGTCCAACCCGCGCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG
 GGGTGCAGGGCCCTGTGAGGAGATTCCGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA
 CACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT
 GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTTCAAGGGGCGAGCTT
 TCCTGGCCAGAGCCAGAGACCCCGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGAGGCAGGCT
 GATGCACCAGGGACAGCTGGCCTGTGGCGAGCCCTGGTGTGAGAGGAGGGGTGCTAACTG
 CTGCCCATGCTTCTATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACAGA
 CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCTGAGGGGG
 CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCC
 TCTGCTGCCCTATCTGACCACCACCTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
 GCGCGCCAGGAGCAGGCATCAGCTCCTCCAGACAGTGCCCGTGACCTCCTGGGGCCTAG
 GGCCTGACAGCCGGCTGATGACGCTCCTGGGGTGTGAGGACCCCTATTCTGCGGGGATGG
 TGTGTACAGTGCTGTGGTGGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCACTGGTG
 CATGAGGTGAGGGGACATGGTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG
 CCCCGCCAGGCCCGCGGTCTTACCGCGCTCCTGCTATGAGGACTGGGTGAGCAGTTTGG
 ACTGGCAGGTCTACTTTCGCCGAGGAACAGAGCCGAGGCTGAGCCTGGAAGCTGCTTGCC
 AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCAAAATGGCATTACTGCCCTGTCTCCCCACCTGTGATGTGTGATTCCAGGCAC
 CAGGGCAGGCCCAGAGCCAGCAGCTGTGGGAAGGAACCTGCGCTGGGGCCACAGGTGCCCA
 CTCCCTCCTGCTGAGGACAGGGGTGTCTGTGGACACTCCCAACCCCACTGTGTAACGAAGC
 AGGCGTCCAGCTTCTCCTCTCTTACTCTTTTACAGATAACAATCAGCCAGCAGCTTGT
 TGAATTTCTTTTTTTGGGGGCGAGCAGTTTTCTTTTTTTAACTTAAATAAATGTTAC
 AAAATAAAA

10017081.102401

FIGURE 49

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV
PGEWFWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAAATELNSWSVVLGSLQREGLSPGA
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPAPRPGMLCGGPQPGVQGPCQGDSGGPVL
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSDEDS
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG
WVLGRARPGAGISSLQTVPVTLTGPRACSRLLHAAPGGDGSFILPGMVCTSAVGELPSCGLS
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP
GSCANISQPTSC

Important features:

Signal peptide:

amino acids 1-15

Homologous region to Serine proteases, trypsin family

amino acids 79-95, 343-359 and 237-247

N-glycosylation sites.

amino acids 37-40 and 564-567

Kringle domains

amino acids 79-96, 343-360 and 235-247

FIGURE 50

CGGGCCGCCCCCGGCCCCATTGCGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCCAGAGTCGCGCGCGCGCGCAGGGGAGCCCTCCACCACGGGGAG
CCCAGCTGTGAGCCGCCTCACAGGAAGATGCTGCGTTCGCGCGGGGAGCCCTGGCATGGGTGT
GCATGTGGGTGAGCCCTGGGAGCACTGTGTTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAAACA
GCTGGTGACAGCTTTGCTGAGGGCCAGGACACAGGGCAGCGCTATGCCAACCGCACGGCCC
TCTTCCCGACCTGTGCGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCG
GACGAGGGCAGCTTCACTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCAGCATGACCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTGAGGCTGAGGTGTTT
TGGCAGGATGGGCAGGGTGTGCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA
GCAGGGCTTGTGTTGATGTGCACAGCGTCTCGCGGTGGTGTGGGTGCGAATGGCACTACACA
GCTGCCTGGTGCACAACCCCGTGTGCAGCAGGATGCGCACRGTCTGTACCATCACAGGG
CAGCCTATGACATTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGTGTCTGTCTGTCTCAT
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG
GAGCTGTACCCCTCCCTACAGCTCCTACCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGTGCCTTTT
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTC
TCCAATGGCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTGCAGGCTCAACATCTCTGGAGCTAGAAAGCTGTTCTCCTTT
CCCTCCTTCCTCCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCAACCCCAACCATGGTGTATTCTGGGGCTGGGGCAGTCTTTCTGGC
TTGCCCTGCGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCG
GATGTCTCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTGTAAACTGGGGGTATATTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALVQVPEDPVVALVGTDATLCCSFSPPEGFSLAQ
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASRLQRVRVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITTCSSYQGYPEAEVFWQDQGQVPL
TGNVTTSQMANEQGLFDVHSLVRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVCWRKIKQSC EEENAGAEDQDGE GEGSKTALQPLKHS DSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCTGTGACCTTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCCTTCTAAGAAGGGGGAGTC
CTGAACCTGTCTGAAGCCCTTTGTCCGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGTGCTTTTGTAGGACTTCTTTCTTGCTTCAGCAACATGAGGCTTTTCT
TGTGGAACCGGGTCTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTGATCCCCTGAACCA
GAAGTGAATAATTGAAGTCTCTCAGAAGCCATTTCATCTGCCATCGCAAGACCAAGGAGGGGA
TTTGTATGTTGGTCCACTATGAAGGCTACTTAGAAAAAGGACGGCTCCTTATTTTCACTCCACTC
ACAAACATAACAATGGTTCAGCCCATTTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAGCTCATCATCTCCTCCTGC
TCTGGGCTATGGAAGAAGGAAAAGGTAATAATCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGCAATGGACCAAGATCCCATGAATCATTCGAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTGAAAA
ACATGGTTCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCTTTTAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTATACAATGTTCTTCTTGCTTTGTTTTTATTTTATATATTTTTT
CTGACTCCTATTTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTCTGATAAGTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTCACTTTACAG
ATATGAAGCTTTGTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCCTCTATTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATATGAAATAGTTTATGTGTAACCTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA
TGGTTGTTGGACCTGACTTGTTAAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAAAAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAG
GCTGAGGCGGGCGGATCACTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA
CCCTATCTCTACTAAAAATACAAAGTAGCCCGCGTGGTGATGCGTGCCTGTAATCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAACTCACTTGAACCCGAGGCCGAGGTTGCGGTAAAGCCGAG
ATCACCTNACGCTGGACACTCTGTCTCGAAAAAAGAAAAAGAACCGGTTAATACCATATNA
ATATGATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTTCAATATTTACTTCTTAAAGGC
TAGCGGAATATCCTTCTGTTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAGATAAAGTAGTAAACCAAGTCTACATTTTCCATTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCAGCACTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTCTA
CTAAAAATCAAAAATTAGCCAGGCGTGGTGGTGACACCTGTAGTCCAGCTACTCCGGGAG
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGTCAGTGAGCCAAAGATTGTGCC
ACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGACAGA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
MRLFLWNAVLTLFVFTSLIGALIPEFEVKIEVLQKPFICHRTKGGDLMLVHYEGYLEKDGS
L
FHSTHKHNNQPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIIPPALGYGKEGKGKIPPEST
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKKGAVVNESHHDALVED
IFDKEDEKDKGFISAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT
 CCAACCATTCCTCCCTTGTAGTTCCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGA
 CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCTTGGCTACCTCGCCCTGCCTTCAGCCT
 CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTACAGTAC
 CTGCCACCCTCAACGCTCTCAATGGCTCTGACGCCCGCTGCCTGCACCTTCAACTCCTGC
 TACACAGTGAACCAAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGAACAACTGCTC
 TGAGGAGATGTTCTCCAGATTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
 ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGGTGATGTCTGAGAAAAGTG
 CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCTGACCGCCACCGTGG
 CCATGGCAAGATCCATCTGCAGGTCTCATGGAAGAGCCCTGAGCGGGACTCCACGGTGG
 CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTTGGTGCTGATGGTG
 GTCAGATGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCAGATGACCTGAAGACCGAGGA
 GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCAAGTAGTGGGTGGCCGGCC
 CTGCAGCCTCCCGTGTCCCGTCTCTCCCTCTCCGCCCTGTACAGTGAACCTGCCTGCTCG
 CTCTTGTGTGTCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCGG
 ACTTCGTATCTCCACCTGACACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
 TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAAGGCTCCACCTGCCAGTCCCTGG
 GGGAGGCAGGAGGCACATGTGAGGGTCCCAAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
 GGAGGGGCGCTGTACCTGCCAGTGTCTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG
 GGAGGGAGGGCTTCTGTGTCTGACAGCGCTCCCTCAGGAGGGCCTTGGCTTGGCAGGCTG
 TGCTCCTCCCTGCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA
 AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCAGGGCACTGACGGAAGCCAGGG
 CTGCAGGCAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
 GCTAGTGGCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
 ACTGGAAGAGCAGCTCCAGGTAGGGGGCATGTTTCCAGCGGGGACCCACCAACAGAGGCC
 AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGTGTAATGCAGGTTGCTGCAG
 GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT
 GAGGAGGCCATGCACAGGGTGGGGCAGCTTCTTGGGGCTTCAGTGAGAATCTCCAGTT
 GCCCTTGGTGGGGTTTCCACCTGGCTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG
 GCATAAGGGGAGGCCTTGGAACTTGAGCTGCCAATGCCAGCCCTGTCCATCTGCGGCCACG
 CTACTCGCTCCTCTCCAAACAACCTCCCTTCTGTTGGGACAAAAGTGACAATTGTAGGCCAGGC
 ACAGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCAAGGCGGGTGGAATTACCTCCAT
 CTGTTTAGTAGAAATGGGCAAAACCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG
 GTGGCGTGTGCTGTAATCCAGCTATTGTTGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG
 GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC
 ATAGAGAGACTCCATCTCAAAAAA

1007031-102401

FIGURE 55

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGLAVVILVLMVVKCVRRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

FIGURE 56

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCCACCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC
TCAATGGCTCTGACGCCCCGCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAAGTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCC

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FIGURE 57

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCCTCAACGTCCTCAATGGCTTTGACGCCCGCCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAAACCCAGCAAGTACGATGTGTTCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAAC TGCTACATCATGAACCCCC

1000

TGCGSCGACGCTGCTACAATAGGGCCCTCCACTCCGCGCTACCGCTGTGGGGCTGCTCCGGATGGCCCTCTCT
TCTCTTGCTGCTGCTAACTGCTGCTCGGAGCCCGAGCTCCGCGCGAGCTACCCCCAGGTGGTGTGGTCT
CTGGTGATTTGGGTAAACCAACTGGAAGCCAGCTGGACGAGCGAGTGGTGCACTACCTCTGCTCCAGAAAGA
CCGAAGAGCTACTTACAACATCTGGCTGGAACCTGGAACCTGCTGCTGCTGTCATCTATGAATGACGTGTGACA
TAGAGCTGGTTTACACAAAACCTACAGGGCCACCCAGTTTCTGATGGTGTGATGTAGCTGTCCCTGGCTTTG
GGAAGACCTCTCTACCTGGAAGTTCTGGAAGCCCGAAGAAAGCGAGTGGGTTCTTAACTTCCACCACTGGTGAAG
GCGCTTGGGCTGGGGTACACAGCGGGTGAAGTGTCCAGAGGGCTCCCTATGACTGGCGCGAGGCCCAAAT
AAAAAGCGGCCCTACTCTGGGCCCTCGCGAGATGTACAGGAGATGTACAGCTGTATGGGGGCCCGCTGGTGG
TGGTTGCCACAGTATGGGCACATGTACACGCTTACTTTCTGACGCGGACCGCGAGGCTTGGAAAGCAAGT
ATATCCGGGCTCTCTGTGCTCAGTGGTGCGCCCTGGGGGGGCTGGCGAAGA CCGTGCCTGCTGGCTCTCAGAG
ACAAACACCGGATCCAGGACTCGGGGCCCTGAAGATCCGGAGAGAGCGAGCTCAGCTGTCTCACACAGCTGGC
TGCTGTCCTTACAACCTACATGGTCACTCAGAGAAGGTTCTGCTGACAGACCCCAATCAATCACTACCTGGGG
ATACCGCAAGTTTCTTCAGGACATCGGCTTTGAAGTGTTCGCTGATCGGAGACACAGAAGGCTGGTGG
AAGCCACAGATGGCCACTTGGCTGACGTGACGTACCTCTATGTGATCTGGCTGCCACACAGCATCTCTACTAT
ATGAGAGCTTCCCTGACGCTGACCTAAAATCTGTTTGGTGAACGGCTAGTGATCTGTAACTTGAAGATGGCC
TCAGTGGCCAGGCTCGGACAGGCCCGACAGGACACAAAGTTGTGCTCAGAGAGCTCGGACAGGAGCATCAT
AGATGTGCGCCACGCGACCTGCTGGCTCTCTGAAATCTGTCTTGGGCCCTGGACTCTGTGTGCCACAGGA
CTCTCTGTGCTCGGCGGTGACCTGCTTGGCTCTGGGGCTCTGAGGCCATGCGCCAGCGTCTTGCAAAATTTGTA
TCCACCATCAAGGCCCCGAATCTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCTTCTCTCT
GTGGCAGTGAAGAGGAAGAGTGAAGTCTAGACTCTAAGGGACACTGAGTGGCAAGATGCTGCTGATGTGGGA
ACTGCTGTGACCTATAGGACTGCTCTCAAGGGTGTGACTGGCTGGGCCCCGTGGCCAGTCCCTGCTGGGCGATG
TGTCCCCATTTCTCTGTGGGTTTCTCATACTGCTACTTGGGCCCTGGGCCCGAGGCTTCTATGAGGGATGTT
ATCGGGCTGTGGTCTGTGACAGAGGTTCCAGGATCGGCTCTGGGCCCTCGGGTGTAGCTTCCCAACACCA
ACGACAGATAGATGCTCCATCTGTGATCTGGGTAGCTAGAGCTGTGGTCTTCTGTGGTCTGGCTGTGGCCAGC
TGACTGGCTCTGGGGCGAGCTGTAGTACTCTGTGACGAGGGGAGTTTGTGTGCTATTTGGTGGTGTCCAGG
CTGGGACACTCATCTCACTCACTACTCCCTTACGACACAGAGATCTCAAGCTCTGATTTGGGACAGAGATGTG
CCCCAGTCCCGCAGGCTGTGTTCCAGGGCCCTGAGTTTCTCGGATGTGCTATTTGGGCCGACCTGAAGCTGTG
CTCCTTCTACCGTGGGATGTGGTTTCAAGGATGAGACGGGGTGGAGCTCAGTGGCTTCTGGAACTCATGGA
GAAAGGGAATCAAGGAAGACGCAAGGAGCTGCTCGAGCTCTCCTGAGTGCACCTCTGTCATCCCACTATGGA
CACTGCGACCTCGCTAGGGTCTCACTAGTACAGTGGGTGACACAGGGCTGAGGATGGGGCTCTATTCAC
CTTGGCCGACAGCCAGCTTAGTGTCTGGGATGAGCCAGAGAATCTGATGGGACCTGAGAGAGCAGGGGTCCC
TAGGGCCCCCTAGGGGCTTCTGTCTGTCGCCAGGAGCTGCATGAGTCTCCCTGTGGAGCAGGCTAGGAGAT
CAGGGCTGCTCTTATGTCAGTGAAGTCTTAAGTGGGTGACGCCAGAGCCAGAGAAGAGGTTACAGCTCTTAGT
GGGTTCCCAAGACGCTTCAAGCTGAGCTAGAGCTGCTCTGCCACAGGTTTCTGTGAGCTGAGTTTCTCTGT
TGATCATAGCTGCTGGCATCTGTCTCCCTCTGTCTCTAGTGGCCCCACAGGGGCTCAGAGCGCTGTATCTGT
GATTCTGGCAATAAAGATCTCTGATGCTGTAAAAAAAATAAAAAAATAAAAAA

FIGURE 59

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVVPFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGFPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI
PVIGPLKIREQQRSVAVSTSWLLFPYNTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLGPF
```

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCGAGCGGGCGACGGCGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCGTGTGCTTGGTCTTCGCCITGATCGTGTCTCCTGCATCTATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTC AACCGCAACGAGGAT
GCCTGCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCTCTGGCCTCGGCCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACCTACCAACAGCCACCCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAATGCCA
GCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGTGAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGACAGGCTCTGTGTCTCTCA
CTCAGGTTTGCTTCCCTGTGCCCACTGCTGTATGATCTGGGGCCACCACCTGTGCCGGT
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTATGGCACTTCTCTCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTTACTTAGGAAGCCTGGGAGGGCAGGGGTGCCCATGGCTCCAGACTCTGTCT
TGTGCCGAGTGATTATAAAATCGTGGGGGAGATGCCCGGCTGGGATGTGTTTGGAGACG
GAATAAATGTTTTCTCATTTCAAAG

1007687-102401

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYGSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDLFLSALWTFWLVGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

FIGURE 62

GAGGCCCTACCCTGCTCCGAGGCCAGGCCCTGACGGGCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCGGTGGCCGAGGCCCCCGAGGTGGCTGGCCGGGACGGAGGGTGTGGCGAGGAACCGGAGCCAGAGGGG
 ATGTTCAAGGCCCTGTGAGGACTCCAGAGAAAAGCCCGGGCTACTCCGCTGGTGGCCCTGTTTGTGCTGCTG
 GCCCTGCTCGTGGCTCGCGGGGGGTGCTACTCTGGTATTCTTAGGGTACAGAGCGGAGGTGATGGTCAGC
 CAGGTGTACTCAGCAGCTGTGGTGTACTCAATCGCCACTTCTCCAGGATCTTACCGCCGGGAATCTAGTGCC
 TTCCSCAGTGAAGAACCGCCAAAGCCAGAGATGTCTAAGAGGCTCATCACCAGCAGCCCGCTGGGAATCTACTAC
 AACTCCAGCTCCGCTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTCAATCTCCAAATCCCCGAG
 CACCGCCGCTGATGTCTGAGCCCGAGGTTGGTGCAGGCACCTGCTGGTGGAGGAGCTGTGTCACAGTCAACAGC
 TGGCTTGGCCCTCCCTACAGGGCCGAGTACGAAGTGGACCCGAGGGGCTTAGTGATCTCTGGAAGCCAGTGTGAAA
 GACATAGCTGATTAATTCACGCTGGGTGTGTACCGCTACAGCTACGTGGGCGCAGGGCCAGGTCTCTCCGGCTG
 AAGGGGCTGACCACTGGCCCTCAGCTGCCTGTGGCACTGCAGGGCCCCAAGGACCTCATGCTCAAAATCCGG
 CTGGATGGACGCTGGCAGAGTGC CGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCTGGAGAAAGAGGCTC
 ATCACCTCGGTGTACGGCTGCAGCCGACGAGGCCCGTGGTGGAGGTTCTGGGCTCGGGGCCATCATGGCGGTC
 GTCTGGAAGAGGGCCCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTCCAGGCCCTGT
 GAAGTGAACCTGACGCTGGACAAAGGCTCGACTCCAGGGGCTCCTCAGCACCCGCTACTTCCAGCTACTAC
 TCGCCCCAAACCACTGCTCTGGCACTCAGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTGATGCC
 TATGCACTGAGGAGGCAGAGTATGATTGCGGTGCACCCAGGGCCAGTGGACATCCAGAACAGGAGGCTGTGT
 GGTCTGCGCATCCTGCAGCCCTACGCGAGAGGATCCCGTGGTGGCCAGGCGGGATCAACATCAACTCACC
 TCCAGATCTCCCTCACCGGGCCGGTGTGCGGTGCACTATGGCTGTACAACAGTCCGACCCCTGCCCTGGA
 GAGTTCTCTGTCTGTGAATGGACTCTGTGCTCCTGCCTGTGATGGGGTCAAGGACTGCCCCAAAGGCTGGAT
 GAGAGAAATCGGTTTGACAGGCCACATTCCAGTGCAGAGGAGCAGACATGCATCTCACTGCCCAAGGCTCTGT
 GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCAGGAAGGGGTGCCATGTGGGACATCAACC
 TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGGCGGCCGACTGCAGGAGCGGC
 TCGGATGAGGAGCACTGTGATGTGGCTCCAGGGGCCCTCCAGCCGATTTGTTGGTGGAGCTGTGTCTCCGAG
 GGTGATGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGTGCACATCTGTGGGGGGCCCTCATGCTGACCCG
 TGGGTGATACAGCTGCCCATGTCTCCAGGAGGACAGCATGGCTCCAGGGTGTGTGTGACCGGTGTCTCTGGGC
 AAGGTGGCAGAACTCGCGCTGGCTCCAGGCTGGAGAGGTGTCCTTCAAGTGTGAGCCGCTGCTCTCCAGCCGCTCAC
 GAAGAGGACGCCATGACTACAGCGTGGCGCTGTGTCAGCTCGAGCAACCGGTGGTGGCTCGGCCCGCTGGCG
 CCGGTGTGCTGGCCCGGCTCCCACTTCTTCCAGGCCGCGCTGCATCTGATTAAGGCTGGGGCTGGGGCGCTTG
 CGCGAGGGCGGCCATCAGCAAGCTCTGTCAGAAAGTGTGATGTGCACTGTATCCCAAGAGGATGCTGTCAAGG
 GCTATGCTTACCAAGTGTGACGACGATGCTGTGTGCGGCTACCGCAAGGGCTGGTGGCTGGGGCTGG
 GACTCAGGTGTGCTCGCTGTGTGTGCAAGCACTCAGTGGCGCTGTGCTTCTGGCGGCGCTGGTGGCGGCTGG
 GCTGTGGCGGCTCAACTACTTCTGGCGCTACACCCGCTCACAGGTGTGATCAGCTGGATCCAGCAAGTGTG
 ACCTGAAGAACTGCCCGCTGCAAAGCAGGGCCACCTCTGGACTCAGAGAGCCAGGGCAACTGCGCAAGCAGG
 GGACAGAGTATTTGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTGTGCTC
 CTGATGTGCTTCTCCAGTGTGTCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGAOCTCCCTGAGGACC
 CAGGCCCAACCCAGCCCTTCTGCTCCCAATCTCTCTCTCCGTGCCCTCTCTCTCACTGTGCTCAATGCAAG
 GCAGTGGCTCAGCAGCAAGAAATGCTGGTCTACATCCCGAGGAGTGTCTGAGTGGCGCCCACTCTGTACAGAGG
 CTGTTTGGGCACTTGGCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGTGCTTAACTTGGGATCTGGGAAT
 GGAAGGTGCTCCATCGGAGGGGACCTCAGAGCCTGGAGACTGCCAGGTGGGCTCTGCTGCACTGTGAAGCCAA
 AAGGTGGGAAGTCTGACTCCAGGGTCTTGGCCCAACCCCTGCTGCCACTGGGCGCTCAGCCACAGCAGCCT
 CACTGGAGGTGAGCTCAGCTGCCCTTGGAAATAAAGCTGCTGATCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGGQGDGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT
YYNSSSVSYFGEGLPTCFFWFILQIPEHRRMLSPPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQQVRLKGPDLHASSCLWHLQGPKDMLM
KLRLLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLLDSQGVLTSTPYFFSYSPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPCTQGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNAGDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRRATFQCKEDSTCIS
LPKVCDGGPDCLNGSDEEQCEGVPCGTFTFQCEDRSCVKKPNPQCDCGRPDCCRDGSDEEHCD
CGLQGPPSRIVGGAVSSEGEWPWQASLQVRGRHICGGALITADRWVITAACHCFQEDSMASVTL
WTVFLGKVVQNSRWPGEVFSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHHFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQQVVV

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTAACAACAGTCGGACCCCTGCC
CTGGAGAGTTCCTCTGTTCGTGAATGGACTCTGTGTCCTGCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCTGGATGAGAGAACTGCGTTTGAGAGCCACATTCCAGTGCAGAGGAGGA
CAGCACATGCATCTCACTGCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACTTCCAGTGTGAGGACCGG
AGCTGCGTGGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGCAGGACCGGCTCGGA
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGATTTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGTGTCAGCTCGACCACCGGTGGTGCCTCGGCCCGCTGCGCCC
CGTCTGCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCTGCATGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCATCAGCAACGCTCTGCAGAAAGTGATGTGCAATTG
ATCCACAGGACCTGTGTCAGCGAGGCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTTCAGCTGGGGCTGGGCTGTGGCCGG
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAAGTGCCCCCTGCAAAGCAGGGGCCACCTCCTGGACTCAGAGAGCCAGGGG
AACTGCCAAGCAGGGGGACAAGTAT

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVFPFGEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTDAVNNTRVVGHISIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIIHKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLCEP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

FIGURE 67

CGGACGCTGGGCGGACGCTGGGCTGGGCAAGGGCCGGGGCGCGGGCCGAGCCACTCTTCCCTCCCCCGC
 TTCCCTGTGCGCTTCGCTGGCTGGAGCGCTGGAGGAGTGGAGCAGCACTCCGGCCGCGCTTGGGGGTGACAGT
 CGGCAAAAGTTTGGCCGAAGAGGAAGTGGTCTCAAACCCCGCAGGTGGCGGACGAGCCAGGGGCGCTCG
 CTGCTCTCGGGCGGGCTGTAGCGAGGGCGCGCCCACTGGCTGCCGAGACCCGGGGCTTCAGGAGCGCGGCCGGGAG
 AGAAGAGTCGGCGCGGACGAGAGAAAACAATCCAAAGTTGGCGAAAGGCACCGCCCTTACTTCCCGGGTGGCG
 CCGCTCTCCGCGCCGACCTTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGCCCCCTGGGAGGGCGG
 CACCAGGGAGCTTGGGCGCGCCGGGCTCCGCGCGACCCCATCGGGTAGACAGGAAGCTTCGGGACCTTTCGG
 GCACCTCTGGACAGCCCGAGTGTCTGTGGCCACCTCTCTCTCTCTCTCTTGGAGGGCTCTTGGCCCATCCAG
 ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGTCTTTAGAAAGTGCAGGGCACCTTACAGA
 GGCCCTCGTGTGGGACGAGCCGACCTTCCCTGGCACTGCACCTGGCTCATCTGGGACGAGGAACAGACTG
 TCACCATCAGGTTCCAGAGCTACACTGGCCCTGTGGCTCAGAGCGCTTAAACCTTACGCTCCCTCTCCAGCCAC
 TGAATCTCCCTGTGTGAGGCACTCCAGCCCTCTGCAGCTGGCCGGGGCAACGTCAACCATCACTTACAGCTATG
 CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCTGTCTCTCTACAGCCAAGATTGGCTGATGTGCGCTGCAGGAAG
 AGTTTCAGTGCTGAACCAACCGCTGTGATCTGTCTGTCCAGCGCTGTGATGGGGTGTATGCTGTGGCGATGGCT
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCGTCCCTCCCTGCTTGAATG
 TCACCTTGGAGGACTTCTATGGGGTCTTCTCTCTCTGGATATACACACTAGCCTCAGTCTCCACCCCCAGT
 CCTGCCATTGGCTGTGGACCCCCATGATGGCCGGCGGCTGGCCGTGGCTTACAGCCCTGGACTTGGGCTTTG
 GAGATGCAGTGATGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCTAGTGTCTACCCACTTCA
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTGTGTCTTACCACAGTGTCTTGGAGCA
 ATGGTGTGGCTTCAATGCCACCTACCATGTGGGGGCTATTGCTTGGCTTGGGACAGACCTGTGGCTTAGGCT
 CTGGCCTGGGAGCTGGCGAAGGCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACCGCTCATGGGACT
 GTGCTGACGGCAGATGAGGAGGACTGCCAGGCTGCCACCTGGACACTTCCCTCTGGGGCTGCTGGCACT
 CTGTTGCCACAGCCTGCTACTGCTGCTGACCGCTGCAACTACGACACTTCTGTGCTGATGGAGGATGAGA
 GACGCTGTGGCATTGGCAGCTGGCAATTTCCGATGCCGGGACGAGAGTGGTGTATGAGACGTGGCTGTGGC
 ATGGGCGAGCAGACTGTGCGGACCGCGAGTGATGAGTGGGACTGCTTATGCTCCCGCGCAGGCTCATTAAG
 CTGCAGTCAATGGCAGCTAGTGTGCGGCTGCTCCTGGTCTATGCCCTGGGCTGCACCTGCAGCTCTATGCCA
 TTGCGACCCAGGATACAGCATCTTGGCCCGGCTGCCATCCCACTGTAGAAGACTTCTTACAGAGAACTCTAATGATA
 ACTCACTCTGGGCACTCTGCTCTCTGCTACAGACTTACCGCAGGATATGACTCCAGAGGTTGGCCAGGTTG
 CCGCGCGTGTGACGGGGCGCGCTGTATGCGAGCCTGTGACCGCTTCCGCGCTGGGGCTTGTCTCCCTCGAA
 CCAACACCCCGCTCGGCGCTTGGGCGAGATCCAGGTCACACTTCTGTGCTCCCTTGGAGCCCTAGATG
 GTGGCACAGGTCCAGCGCTGAGGGCGGGCAGTGGGTGGGCAAGATGGGAGCAGGCAACCCCACTGCCCATCA
 AGGCTCCCTCCCATCTCTAGCAGCTTCCAGCCCCCACTACTGTCTTGAAGCCCGAGGGCCACTGCCCTCAC
 TGGCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCGCTGGAGGGCGCGCTGTGTGCCAGCTGGGCGCCC
 CAGGACCAACCGGAGCCCCCTGGACCCCAACAGCAGTCTTGGCCCTGGAGATGAGGACGATGTGCTACTGG
 TGCACCTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTTCTTACTTGGGGGACTGGGG
 CTCTACTGAGGCTCTCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTGAAGGTGGGTGAGCTCTCCCTCC
 ACCACTTCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCTCCCGTGAACCTATGTAGCTCTATAAAGT
 TAAGTGTCCCTCAGGCGAGGAGGGGCTCACAGAGTCTCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT
 TCACCAACCACTGCTCCCGACGCCACCACTTTGGGTGGCTGTTTTTAAAGATAAAGTTCTTAGAGGATCAT
 GGTCTGGACACTCCATCTTGCACAACTTACCCAAAGTGGCCTTAAGCACCGGAATGCCAATTAACATAGAGA
 CCTCCAGCCCCCAGGGGAGGATTGGGCAGAACTGAGGTTTTGGCATCAACAACTCCCTCTACAGGGGCTGG
 CTCACAAAAAGAGTGCAACAAATGCTCTATTCCATAGCTACGGCATGTCTCAGTAAGTTGAGGTCAAAATAAA
 GGAATCATACATCTC

1007662-1007661

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVQGTLLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSPLQLISLCEAPPSPQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDCGVDACGDCGSDGACSSDPFPGLTPRP
VPSLPCNVLTLEDYFGVFSSPGYTHLASVSHPPQSCHWLLDPHDGRRLLAVRFTALDLGFGDAVH
VYDGPGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSDWCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCDKCVYETWVCDGQPD CADGSDWDSCS
YVLPKRVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY
GQLIAQGAIPPVEDFPPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRLLMRRLLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLGGPPGPTRSPPGPHTAV
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCGTAACCATATATTGTTATCACTGGATTGAAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAAATGAAGTGTTATTTTGGCCTTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAGAAGTTTGTAAATTTTATATTACTTTTTAGTTTGTACTAAAGT
ATTAAACATATTTCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL
```

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCCGA
TGGATAACGTGCAGCCGAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGATTATTTGGCCCTTGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNTTGCCGAC

10017031-102401

FIGURE 72

CAGCCCCGCGCGCCGCGGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCTGCGCGCGCCCCGGAGCTGGCCCCGCGCCCTTCACGCTG
CCCCCTCCGGGTGGCCGCGGCCACGAACCGGTAGTTGCGCCACCCCGGGACCCGGGACCCC
TGCCGAGCGCCACGCGCAGCGCTTGGCGCTCGCCCTGGAGCCTGCCCCTGGCGTCCCCGCGG
GCGCGCCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGAACCCCCGCGAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACCTTTCGCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTCTTTTGGCTGGGATTAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGGCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGCGCTTGCC
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG
AAATTGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTATGCGGTGGTGG
AAGCTGTGGCCGCGCATCTCTGATTCAGAAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGTGGACGAATTCGAAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTATTCCGTATCACAATCCTGCCTCAGCTTACATTCAGC
CCATGATGGGGGCCGCGCTGAATTATGAATGTTACCGATTCCGGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTACGTCACTCTTCGACAGAGCCAGAA
GAGGTGGCTTCGACGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCCTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCGTCAGCCCTGACCTCGTCA
ATGATGAGTCCTCTCTGGTCAACATCGCTGGAATGAATAGCCAGGCTGACCTCAAGCAA
CCATGAACCTCAGCTATTAAGAAAATCACATTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGCTCTTCAATCTCTGTTCTGCTCCAGATGCCCTCTAGATTAC
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCTACTTCCAAGAAAAATAATTAA
AAAAAAACTTCATTCTAA

FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVVKYTOGSGWTGFGEDLVTI PKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS
LVLGGIEPSLYKGDIIWYTPIKEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDVAVVEAVARASLIPEFSDGFWTGSQ LACWTNSETPWSYFPKISIIYLRDENSSRSFR
ITILPQLYIQPMMGAGLNYECYRFGISPTNALVIGATVMEGIFYVIFDRAQKRVGFAASPCA
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLPPRC
QRRPRDPEVVNDESSLVRHRWK

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCTTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCTTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGAGCCGGAGGCGCGGCC
GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGCTGAAGGCCCGCCGCTGCGGCGGCATGGGCAACCTGCGGGGCGCAGCGCCGTGG
TCACGGGCGCCAAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGCTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGGAACCGTGAGGCGTTTAACTGCTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCGTAAGGCATGTGCCCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCCACTGTTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGCGAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGGAGCTCGCCCAACAGCTTGAGGCCACTGGCGCTCACCTGTATGCAGCCCAAC
CAGGGCCTGTGAACCTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCACTTTTG
CGCCCATTTGGCTTGGCTGGTGCTCCGGGCAACAAGAGGGGGTGCCCAAGACACCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGGCAACTGCCATGTGGAAG
AGGTGCCCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCGATGAAGACCCCAAGTCTGAGGACTC
AGAGGCCCCATCTTCTCTAAGCACCCCCACCCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTGAGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT
GAAAACTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTGTGATCTTGACCTC
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCTTATTGATTCTG
ATCAGCTCTGAGCAGAGGCAGGGAGTTTGCAATGTATGCACTGCCAACATTGAGAATTAG
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG
GAATTAGGCTCCCCAGCTAAGGGACTCGCCTAGGGTCTCAGTGTAGGTAGGAGGAGGGCGCTG
GGATCTGAACCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAGGGCTGGGTCATCTGTATCTGAAGCCCTCGGAATAAAGCGGTTGACCGCCAAAA
AAAAAAAAAAAAAAAAA

FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDLDFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFRLHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPCEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSQSSPDLSKMTHRIQAKVEP
EIQLS

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

FIGURE 76

GGAGGAGACAGCCTCTCGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGACATGGCTCAG
 GACTCCCCGCCCCAGATCTCTAGTCCACCCAGGACAGCAGTGTTCAGGGGCGCTGGCCCTGCCAGGATGAGCTGC
 CAAGCTCTCAGGCCAGCCACCTCCACCATCCGCTGTTGCTGAATGGGAGCCCTTGAGCATGGTGGCCAGAC
 CCAACACCACTCTCGCTGATGGGACCTTCTGCTGCTCAGGCCCTGCCCGGGGACATGCCCCAGATGGCCAG
 GCCCTGTCCACAGACATCGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCCAGCGATCAGCAGAGGCGCT
 CGGCTCTCTGGGCTCTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGGACATGTGTGGCTGTGGTGGGTGAGCAG
 TTACTCTGGAAATGGGGCGCCCTCGGGGCCACCCAGAGCCCAAGTCTCATGGTGGAAAGATGGGAAACCCCTG
 GCGCTCCAGGCCGGGAAGGACACAGTGTCCGGGGGCTCCCTGCTGATGGCAAGCAGAGAGAGATGACGAGGCG
 ACTTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGTTTCCATCCAGGAGCCC
 CAGGATACACAGGAGCTGTGGAGCTTCTGCGCTGTGCGAATTTCAGTGGAAATGTGACACTGCTGTAACCCGGAT
 CTGTGACAGAGGCCCAAGCTTAGACCGCGGCTGTGGCTCAGCTGGAAAGTTCAGTGGCCCTGCGCTGCTGCCCAA
 TCTTACACGGCTTGTTCAGGACCCAGACTGCCCGGGGAGGCCAGGAGCTCCGTGGGACAGAGGAGCTGTGCTGCC
 GGCTGGCAGAGCGCAGAGCTTGGAGGCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCTCTGGC
 CGGCTCGAGGCGCTGACAGCAAGCTGCTGCTCTGAGGCTGCCGGAAAGTGGCCAGTGCCCACTCAGGAA
 GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCAACCTGCTGAAAACCAATGGCATC
 ATCCGTGGCTACAGGCTGTGGAGCTGGGCAACACATCACTGCCACAGCCAACCTGGACTGTAGTTGGTGAGCAG
 ACCCACTGGAAATGCCACCATGATGCCAGGCTCTTACTGCGTGAGTGGCTGAGCTCACTGGTGTGGAGCT
 GGGGAGCCCAAGTACAGCTGTCTGCTCTCTTTAGAGCAGGCCATGGAGCAGCCACCAAGAACCCGATGAGCAT
 GGTCTCTGGACCTCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCTGAGGCTTATGGCACTGTGGTGTGTGACCT
 TGGCTGTCTTCTGGGACCGCCGCTGTGTATCCACGCCCGGCGCAGGCTAGGGTGCCACTGGGCCAGGCTGT
 TACAGATGATCCAGTGAGGATGCCATCTTAAACACAGGATGGATCACAGTCACTCCAGTGTGGCAGACAT
 TGGCGTTCACCTCTGGCTCTCGGGAGCTGAGCAGCAGCAGCAGCTCAGCAGCTGGCTGGGCGGGATGGCCGG
 GACCCACTAGACTGTGTGCTGCTCTCTGAGCTCCCGAAGCCCGGCTGCCCTGCTTCCAGACACC
 AGCACTTTTATGCTCTCCCTCATCGCTGAGCTGCCCTCAGTACCCAGCAGGCCAAAGTCCCAAGTCCCAAGT
 GTCAGSGCCTCCACCCAGCTGGGCCAGCTCTCCAGGCCCTGTTCAGCTCAGACAGCTCTCAGCCGCAAG
 GGCATCTCTTCTCCCGCTTGTCTCTGSCCCCTGCAGAGGCTTGAAGGCCAAAGAGACAGGAGGTGCCAGT
 GCGAACAGTCTCCCACTGCTCCGGGCGAGCCACTCTTGGAGCTCCAGCACTCCCTCTTCTCATGAAACTCC
 AAGAACCTTTCCCAAGGCCAGGAGCTGTGCCCAAGCTCTGGTGTGCTGGGGGCTGGGACCGGAACTCTCT
 AGCTCTCTCAATGAGCTGTGTTATCTGCTCATCTCCCTCCAGCAGCTCTTCTCTGTCAGCAGGCCCATCC
 AGTCAACAGACCCAGCTCCGCTGGCAGCAGAGGCTCCCTCTCTCATCTGTCGACAGGCCCATCCCATC
 CTTAGCCCCCTGAGTCCCCCTTAGCCCCAGGCTCTTCCCTCTCTGCCCCAGCCAGCTTCCAGTCCGCTGTCC
 A3CTCTCTCATGTCTCTCTGGGGAGGATCAAGACAGCGTGTGACCCCTGAGGAGTATGCCCTGTGCTTGGAA
 GGTATCATCAGCGTCCCAACAGCTCAGAGTTTACGGACATGGGAGGACTGGAGAGGGGTGGGGCCCAAGGGG
 G8AGTCTGTCTGTGCCCACTCGGCTGCTCTACCCCCACCCCCAGCGAGGCTCTTATAGCCAAATGTTGGGGC
 TCACTCTCAGGACAAATGCGCGCCAGCGCCAGAGCCCTTGTCACTCTCCGATGGCTCTTCTCTGCTGAT
 GCTCTCATAGATGCTCATCACTTCCCTCCCCAGGATGAGATCTTCTGACCCCCCACTCTCCCTGCCCTG
 TGGAGTGGAGGCCAGATGTGTTGGAGACATGGAGGTGAGCCACCCAGCGCTGGGAGGGGGATGCTCTCCC
 TGGCCCCCTGACTCTCAGATCTGTCTCCAGAGAAGTCACTGCTCATGTGATGCCCAAGGCTGGTGTCTCTCT
 GTAGATTACTCTGAAACCGTGTCTCTGAGACTTCCAGACGGGAATCAGAACCACTCTCTCTGCTCCACCCAAAG
 ACTGGGCTGTGTGTGTGGGTCTTGGGCTGTGTTTCTGAGCTGGGTCACCTTCCCAAGCTCCAGAGGCT
 TTCTCCCTCAGCATGTGTGAAACAAATGAAACAAATATAGAGCAAAGTCACTGAGCTGGAGCCCTCAGGAGCAA
 ACATCATCTCCACTGACTCTAGGCCACTGCTTTCTCTCTGTGCCATCCATCCCAACCAAGGTTGTTTGGC
 CTGAGGAGCAGCCCTGCTGTGCTCTTCCCCCACTGATTTGGATCAGAGAAAGTGGAGGAGCCAGAGTCCCTTT
 GTGGAGGACAGGATGGCTGCTGGGAGAGGGCTGTGGAGGAGGAGCTTCTGGAGCCCTCTCAGCTTACTCT
 GGGCCCCCTCTCTAGAGAGAGCTCAACTCTCTCCCACTCACCATTGAGGAAAGAAATATATGAATGCCACTG
 AGGCACTGAGGCCCTACTCATGCCCCAAACAAAGGTTCAAGGCTGGGTGAGCAGGATGCTGAAGGAGGGAGG
 TATGAGACCGTAGGTCAAAGACCATCTCGTACTGTGTCACTATGAGCTTGAAGAAATTTGATACCATAAAT
 GGTAAAAA

10017081.102401

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPQILVHPDQLFQGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLP
DGTLLLLQPPARGHAHDQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAESDEGTYMCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLINPDPARGPKRPAPVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRTSLDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSRIGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSPTPARPSPQVPAVRRLPPQLAQLSSPSCSSSDSLCRRGLSSPRLSLAPAEA
WKAKKKQELQHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS
SSNELVTRHLPAPLFPHPETPTTQSQQTQPPVAPQAPSSILLPAAPILSPSPSPQASS
LGGPSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLEPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPVVDS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCTGCTGCT
CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTTGAAGGGGACACTGTGT
CCTTGCACTGCACCTACAGGGGAAGAGCTGAGGGACACCCGGAAGTACTGGTGCAAGGAGGT
GGGATCCTCTTCTCTCGTGTCTTGGCACCATTATGTCAGAAGAAGAAGGCCAGGAGACAAT
GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCCTGTGGA
ACCTCACCTTGCAGAAGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGGCCCGATGAG
TCTTTACTGATCTCTCTGTCTGCTTTTCCAGGACCCCTGCTCTCTCCCTCCCTTTCTCCAC
CTTCCAGCCTCTGGCTACAAACAGCCTGCAAGCCCAAGGCCAAGCTCAGCAAAACCAGCCCC
CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAAGCAGGGGAAGACAGGG
GCTGAGGGCCCTCCATTGCCAGGGACTTCCCACTACGGGCACGAAAGGACTTCTCAGTACAC
AGGAACCTCTCCTCACCCAGCGACCTCTCTCTGCAAGGAGCTCCCGCCCCCATGCAAGC
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
GTGTCATCCCAGTGGTCCGCATCTGGCCCCAGTCTCTGGTGTCTGCTGAGCCCTTCTGTGAGC
CTCAGGCCCTGATCGCCCTTCTGAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCTGGAGGAAAGGAAGCC
CCTTCCAGGCCCTTGAAGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
GAAGCAGTATGGCTGGCTGGATCAGCACCGGATCCCGAAAGCTTTCACCTCAGCCTCAGAG
TCCAGCTGCCCGGACTCCAGGCTCTCCCCACCTCCCGAGGCTCTCCTCTTGCATGTTTCCA
GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGCTCTTCCGGCTG
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
CTCATGCCCAGTGTGGGACCTGCTTCTCTCCACTCCAGACCCACCTTGCTTCTCCCTGCC
TGGCGTCTCAGACTTAGTCCACGGTCTCCTGCATCAGCTGGGTGAGAGGAGCATGCT
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTTCAGGAAGCCT
GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGAG
GACTCTGAATTTCAACAATGCCAGTGACTGTGCACCTTGAGTTTGAAGGCCAGTGGGCCCTG
ATGAACGCTCACACCCCTTCACTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCCC
CAATAGACTGCTGCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCCTGCTAAG
TCCAGGCCCTTGGTCAGGTGACATTTGCAGGATAAGCCAGGACCGGCACAGAAAGTGG
TTGCCCTTTCATTTGCCCTCCCTGCGNCATGCCTTCTTGCTTTTGAAGAAAAATGATGAAGA
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCCTATGGGTTCTGGTGGCTAGAGA
GAAAAGTAGAAAAACAGAGTGACAGTAGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
GCACAACACTACTATTTTTCCTTTTCCATTATTAATGTTTAAAAAGACAGAATCTCGTGCT
GCTGCCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCCGCTCTCTGGGTTCAAGTGATT
CTTCTGCTCAGCTCCCGAGTAGCTAGCTGGGATTACAGGCACGCCACCACCACTGGCTAATT
TTTGTACTTTTAGTAGAGATGGGGTTTACCAGTGTGGCCAGGCTGGTCTTGAACCTCTGAC
CTCAATAGAGCTCTCTGCTCAGTCTCCCAATTTGCCGGGATTACAGGCATGAGCCACTGTG
TCTGCCCTTATTTCTTTAAAAAGTGAATTAAGAGTTGTTAGTATGCAAACTTGGGAAG
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCAACCATAGTCTCACCAGAGACTATCAT
TATTTTCGTTTGTGTACTTCTCTCCACTCTTTCTTCTTCAACAATTTGCCGGTGTCTCT
TTTACAGGCAATATCTGTGTATATAACAATTTGTATCTGCTCTTTTCCACTTATCTGTTCT
ATCACTTTATCCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA
GCTGCATAAAAAAAAAAAAAA

10037084.1.12401

THE BENTLEY

<subunit 1 of 1, 332 aa, 1 stop

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
 GTIYAEEBEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDQAGEYWCVEKRGPDSELLISLHV
 FPGPCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSFGLYPAATTAKQKGTGAEPPLPG
 TSQYGHERTSQTGTSPHPATSPAGSSSRPFMQLDSTSAEDTSPALSSGSSKPRVSIPIVRI
 LAPVLVLLSLLSAAGLIAFCSHLLLRKEAQQATETORNEKFWLSRLTAEKEAPSQAPEGD
 VISMPPLHTSEELGFLGSFVSA

Signal peptide:

Transmembrane domain:

amino acids 248-269

amino acids 96-99

amino acids 104-113

amino acids 13-128

FIGURE 80

TTGTGACTAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACACGAGGCTGGTGAGCTGCCTGTCTATCCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCGCCGGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAAGTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC
TTATTTCAACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGACGCAACCTCACCCGAACGTCCCAAC
GTGTGCCGGATGTA CTGCTCAGATTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCTGCACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGGTTGAACGTGAAA

FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNPNLKDTVICAMKITQEPQGLGY
WEAWRHHCQKDLTEWVDGCF

Important features:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 67-72

Homologous region to Alpha-lactalbumin / lysozyme C proteins.

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCCGTGCCTCGGGCGGGCGCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCTGCGTTTC
 GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCGCGAGCAAAGTGGCTGTACCTGGCCA
 AGCTGTGTCGTCGTTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCTGATC
 CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
 CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCGGGAACCGGCGCTGGAACTGCTCCACAC
 TCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCCTTCGTG
 TACGCCATCTCTTCGGCAGGTGTGGCCCTTGCAAGTGACGCGGGCGTGCAGCAGTGGGGAGCT
 GGAGAAGTGCGGCTGTGACAGGACAGTGATGCGGTCAGCCACAGGGCTTCCAGTGGTCAG
 GATGCTCTGACAAACATCGCCTACGGTGTGGCCTTCTCAGAGTCGTTTGTGGATGTGCGGGAG
 AGAAGCAAGGGGGCTTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCCGCGCAG
 GAAGGCCATCTTGACACACATGCGGGTGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG
 AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCGGCAGGTGGGTGACGCACTGAAGGAG
 AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCGCGTGGGCTCTCCAGGGCACTGGTACC
 ACGCAACGCACAGTTCGAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG
 ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGTTGGGCAGAGGGGGCGCACATGCAACAAG
 ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCGCGGCTTCCACACGGCGCA
 GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGCTGCTTCGTCAAGTGCCGGC
 AGTGCCAGCGGCTCGTGGAGTGCACACGTGCCGATGACGACCGCTGCCTAGCCCTGCGCCGGC
 AACCACCTAGTGGCCAGGGAAGGCCGATAATTAAACAGTCTCCACCACCTACCCCAAGA
 GATACTGGTTGTATTTTGTCTGTTTGGTTTGGGTCTCATGTATTATTATGCGCGAA
 ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCTCCCAAAGCCTGGGCCTTTGTGGCT
 GCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
 CTAGTTGTTATCTGTGTCGCTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT
 TACCACCACATGGCTACTGACCGGTGCATCGGGGAAGAGGGGGCTTATGGCAGGGAAAATA
 GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAACCTCCTCAGCACACA
 TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG
 GAACAAGCAGATACAGGTCAAGGCACACAGTTTCATTTAGCCCTTACATGGACAGCTAGA
 GGTTTCATATCTGTGGGTCTTTCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA
 GTCCACCTTAGAACCAGCCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCC
 CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT
 TGCAGTCATGCCCCAGTCACTTTTACAGCGCTGTTCTCCATGAACTGAAAAACACACAC
 ACCTGCGAGA
 GAGAGGGAGGAAGGGCTGTGCCTTTGCAAGTCATGCCGAGTCACCTTTCACAGCACTGTTCTC

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLSRLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLE
VMDSVRRGAQLAIEECQYQFRNRWNCSTLDSLVPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSNIAVGVAFSQSFDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLESPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGC**CA**TGGACACCACCAGGTACAGCAAGTGGGCGGCAGCTCCGAGGAGGTCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGCTC
ACCACAGTCTCTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTGCGGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGA**ACT**GCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACA**ACT**CCTGCGAGCCG
TGCCCCACGTCGTGGCTGTCTTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGCC
TGGATGAGCAGGGCTTCTCTACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCCTGAGG
GCTGTGCGCCATCTGGGCAAGGTT**CAGGGCT**ACCAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAAC**CAGGGAGAGCCCA**TGACGCTTGGGGGCGCGAGAACTGTGT**CATGATG**C
TGCA**CACGGGGCTGTGGAACGACG**ACCCTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACA**ACTGCTGA**CCCCGCCAGTGCCCTGGAGCCGCGCCCATTGAGCATGT**CGTA**
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCCT
CATCCACCGCTGCTGAGTCTCAGAA**CACTTGGCCCAACATAG**CCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCTAACTCCA**CTCACG**CAGACCCAACTAACC
TCCACTAGCTCCAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTCTCGCATTTTCCACCAA**ACTGGA**
AGCTGTTTTTGACGCCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

<subunit 1 of 1, 293 aa, 1 stop

MDTTRYSKWGGSSSEVPGGPWGRVWHVSRRLPLFLALAVLVTTVLWAVILSILLKASTERAA
LLDGHDLRLRTNASKQTAA LGALKEVGDCHSCSGTQAQLQTTRAE LGEAAKLMEQESALR
ELERERVQTGLAEAGRIGVEDRVTLELFRALAEAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW
AAAQDHCADASAHVLVGVGLDEQGLFLTRNTRGRGYWGLGRAVRHLGKVQYQWVDGVSLSFS
HWNQGEPCNDAGRENCVMMHLTGLWNDAPDCSEKDGWICEKRHNC

Type II transmembrane domain:

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
 GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCACGTCTATCTGCCTCTCG
 CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTGGCCGGCCCCGG
 GCGCCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC
 CGCGCTCCCGCTGCTCTGCGCGGGTGATGGAAAACCCAGCCCGGCCGCCCTTGGGCAAG
 GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC
 CATCTGTTCCGCCAGAGCCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
 CGGCCTTCCCAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCTGCTGCTGGGG
 GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTACGTAAACGGGCTGCG
 CGACTTTGCGGAGCGCGGCGAGGCCCTGGGCGCTGTATGAAGGAGATCGAGGCGGCGGGGAGG
 CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCGCTCCCGACGGCACCCGGGCAGACG
 TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGTGGTCTCGTTTGTGGTGCGCATCGTGCC
 CAGCCCCGACTGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGTTTGGCGGG
 AACAGGCGGCGCTGGACCTGTACCCCTACGACGCGCGGACGGACAGCGCTTCACCTTCTCC
 TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCTCCTCTCCAG
 CCACCCGGCCAACTCCTTCTACTACCGCGGCTGAAGGCCCTGCTCCCATGCCAGGGTGA
 CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCGCCCCAGTCTGCCCAGC
 AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAAACGCGCTGGACTGCGAGGTCTC
 CCTGTGGTCTGCTTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
 CTCGTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCTGCCCCGAGCTCGAAGAAGAG
 GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGAGCCCTTGGGCCCCCG
 GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGTGACAGGCGGCCGAGGGCACAGGG
 GGTTCGCGCTGCTCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
 CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTCCCAACCTTGCTTCTTAGGGG
 CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCTGCAGGATAAAGTCATCCCCAAGGCTC
 CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGTCTGCTCCAGGAGATTGTCTCTTATCG
 TCCAGGGGCTTGCTCCCAGCTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG
 AGCCCACTCTCCCGAGGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGCGG
 TTTTCGAAGCGTCAGTGTTTCCATGTTATGGATCTCTGCGTTTGAATAAAGACTATCTCT
 GTTGCTCACAAA

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